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LOCUS Sequence 2 from Patent WO0159153.
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ACCESSION AX211346
VERSION AX211346.1 GI:15523729
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Jansen, H.W., Brueggemann, A., Heitsch, H. and Goesele, H.
AUTHORS Method for identifying substances which modulate the activity of
TITLE hyperpolarisation-activated cation channels
JOURNAL Patent: WO 0159153-A 2 16-AUG-2001;
Aventis Pharma Deutschland GmbH (DE)
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LOCUS AX348086 3459 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 3 from Patent WO0202630.
ACCESSION AX348086
VERSION AX348086.1 GI:18614193
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
REFERENCE 1 Strijbos, P.J., Bates, S.G., Gloger, I.G. and Davies, C.G.
AUTHORS New use
TITLE Patent: WO 0202630-A 3 10-JAN-2002;
JOURNAL SMITHKLINE BEECHAM PLC (GB)
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LOCUS
DEFINITION
AC139548
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

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SEQUENCE, 17 unordered pieces.
AC139548
AC139548.2 GT:28460954
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Homo sapiens (human)
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 133193)

Birren,B., Nussbaum,C. and Lander,E.

Homo sapiens chromosome 15, clone RP13-642K1

Unpublished

2 (bases 1 to 133193)

Birren,B., Nussbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Boguslavskiy,L., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collamore,A., Cook,A., Cooke,P., Corum,B., DeArelano,K.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulne,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schupack,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (05-FEB-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 133193)
Birren,B., Nussbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Boguslavskiy,L., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collamore,A., Cook,A., Cooke,P., Corum,B., DeArelano,K.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulne,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
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Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schupack,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (21-FEB-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 21, 2003 this sequence version replaced gi:28209588.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RW/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information
Center project name: L29456
Center clone name: 642_K_1
----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 127247 bases at least Q40
Consensus quality: 130023 bases at least Q30
Consensus quality: 130882 bases at least Q20
Insert size: 138000; agarose-fp
Insert size: 131593; sum-of-contigs
Quality coverage: 21.9 in Q20 bases; agarose-fp
Quality coverage: 22.9 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 17 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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325 1321: contig of 997 bp in length
326 1421: gap of 100 bp
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2425 2524: gap of 100 bp
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3226 3324: gap of 100 bp
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3326 4509: gap of 100 bp
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7621 7720: gap of 100 bp
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QY 724 AGCCGGGTGACTACATCATTCGCGGAGGACCATCGGAGGAGATGATGATCTTCAATCCAGC 783
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QY 784 ACGGGGTGCTCAGCGTCTCACTAAGGGCAACAGGAGATGATGATGATGATGATGATGATGAT 843
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RESULT 10
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LOCUS Homo sapiens chromosome 15, clone RP11-30N16, complete sequence.
DEFINITION AC021413
ACCESSION AC021413
VERSION AC021413.16 GI:27476161
KEYWORDS HTG
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 199198)
AUTHORS Birren, B., Nusbaum, C. and Lander, E.
TITLE Homo sapiens chromosome 15, clone RP11-30N16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 199198)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

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Matches 1278; Conservative 7; Mismatches 45; Indels 10; Gaps 5;	4	181506	Qy	1144	AGTGGGCTCAGCGCGTGGGCTCTTTCGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	1203
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424	Qy					

RESULT 11
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 DEFINITION Ion channel compound gated by brain or heart cyclic nucleotide and utilization thereof.
 ACCESSION BD139757
 VERSION BD139757.1
 KEYWORDS JP 2002508930-A/4.
 SOURCE unidentified

ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 1790)
AUTHORS Kandel,E.R., Santoro,B., Bartsch,D., Siegelbaum,S., Tibbs,G. and Grant,S.
TITLE Ion channel compound gated by brain or heart cyclic nucleotide and utilization thereof
JOURNAL Patent: JP 2002508930-A 4 26-MAR-2002;
COMMENT THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
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PN JP 2002508930-A/4
PD 26-MAR-2002
PF 23-DEC-1998 JP 2000525534
PR 23-DEC-1997 US 08/997685,28-MAY-1998 US 09/086436 PI
ERIC R KANDEL,BINA SANTORO,DUSAN BARTSCH,STEVEN SIEGELBAUM, PI
GARRETH TIBBS,
PI SETH GRANT
PC C12N15/09,A61K9/08,A61K9/12,A61K9/16,A61K9/20,A61K45/00 PC
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QY 124 GGATCTGCATCTCATCAGCATGATGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 183
DB 660 GGATCTGCATCTCATCAGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 719
QY 184 TCTGTGTGCCATGCTGTCAGGAGCTTCCCGCGCAACTGCTGGGTGTCCATATGGCATGG 243
DB 720 TCTGTGTGCTATGCTGTCAGGAGCTTCCCGCGCAACTGCTGGGTGTCCATATGGCATGG 779
QY 244 TGAACCACTCGTGGAGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 303
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QY 424 TCCAGTCCGTGGACTCTCTCGCGCGCCAGTACCAGGAGAGTACAGCAGGTGGAGCACT 483

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DEFINITION AR307665
ACCESSION AR307665
VERSION AR307665.1 GI:31698370
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1790)
AUTHORS Kandel,E.R., Santoro,B., Bartsch,D., Siegelbaum,S., Tibbs,G. and Grant,S.
TITLE Brain cyclic nucleotide gated ion channel and uses thereof
JOURNAL Patent: US 6551821-A 11 22-APR-2003;
FEATURES Location/Qualifiers
1..1790
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Query Match		89.0%; Score 1194.4; DB 6; Length 1790;	
Best Local Similarity		98.9%; Pred. No. 1.1e-150;	
Matches 1234; Conservative		0; Mismatches 11; Indels 3; Gaps 3;	
QY	4	TCGGCTTACCAAGATCCTCAGCCTCTCGCGCTGCTGGCTCTCTCAGCCCTGATCCGCT	63
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SOURCE Homo sapiens			
ORGANISM Homo sapiens			
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
1 (bases 1 to 127422)			
Birren, B., Nusbaum, C. and Lander, E.			
Homo sapiens chromosome 15, clone CTD-209012			
Unpublished			
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Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,			
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Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.			
Direct Submission			
Submitted (31-OCT-2002) Whitehead Institute/MIT Center for Genome			
Research, 320 Charles Street, Cambridge, MA 02141, USA			
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Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,			
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8744 CTGCTGGGCGCGCTGCGCTGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 8685
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1322 GCACCTGCHGCNCTCACCC 1342
Db |||||
8684 GCACCTGCGCGCGCTCACCC 8664

RESULT 15
AX647819
LOCUS AX647819 2125 bp DNA linear PAT 05-MAR-2003
DEFINITION Sequence 2011 from Patent EP1270724.
ACCESSION AX647819
VERSION AX647819.1 GI:28802445
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Suwa, M., Arai, K., Akiyama, Y. and Aburatani, H.
Guanosine triphosphate-binding protein coupled receptors
Patent: EP 1270724-A 2011 02-JAN-2003;
National Institute of Advanced Industrial Science and Technology
(JP) ; Center for Advanced Science and Technology Incubation, Ltd.
(JP)

FEATURES
Location/Qualifiers
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ORIGIN
Query Match 88.8%; Score 1191.6; DB 6; Length 2125;
Best Local Similarity 95.2%; Pred. No. 2.5e-150;
Matches 1276; Conservative 7; Mismatches 47; Indels 10; Gaps 5;
Qy 4 TGCCTTCACCAAGATCCTCAGCCCTCCGCGCTCTGCGCTCTCAAGCCCTGATCCGCT 63
Db 688 TGCCTTCACCAAGATCCTCAGCCCTCCGCGCTCTGCGCTCTCGCGCTCTGATCCGCT 747
Qy 64 ACATCCATCAGTGGGAGGAGATCTTCCACATGACCTATGACCTGCGCCAGCGGCGATGA 123
Db 748 ACATCCACAGTGGGAGGAGATCTTCCACATGACCTATGACCTGCGCCAGCGGCGATGC 807
Qy 124 GGATCTGCAATCTCATGAGATGATGCTGCTGCTGCTGCTGCTGCGCCAGCGCTGCTGCT 183
Db 808 GGTTCGCAACCTCATCAGTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 867
Qy 184 TCCTGGTCCCATGCTGAGGACTTCCCGCGCAACTGCTGGGTGCTGCTGCTGCTGCTGCTGCT 243
Db 868 TCCTGGTGGCATGCTGAGGACTTCCCGTGAACCTGCTGGGTGCTGCTGCTGCTGCTGCTGCT 927
Qy 244 TGAACCACTCGTGGAGTGAATGTACTCTTTCGCACTCTTCAAGGCCATGAGCCACATGC 303
Db 928 TGAACCACTGGTGGAGCGAATGTATTTCTTTCGCACTCTTCAAGGCCATGAGCCACATGC 987
Qy 304 TGTGATCGGGTACCGCGCGAGCGCGCGAGAGATGACGGAATCTGCTGCTGCTGCTGCTGCT 363
Db 988 TGTGATTTGGGTATGGCGCGAGCGCGCGAGAGCATGACGAGCATCTGCTGCTGCTGCTGCT 1047
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Qy 424 TCCAGTCTGCTGAGTCTCTCG 483
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Db 1165 ACATGCTCTCCACAAAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1224
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Qy 664 CCAAGCGCGACCCCAACTTGTCTGAGCGCATGCTGACCAAGCTCAAGTTCAGAGTCTTCC 723
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Qy 784 ACAGCGCTGCTCAGCGTGTCTCACTAAGGCGCAACAAAGAGATGAAGTGTCCGATGCTCT 843
Db 1462 ACAGCGCTGCTCAGCGTGTCTCGTAAGGCGCAACAAAGAGATGAAGTGTTCGATGCTCT 1521
Qy 844 ACTTCGGGAGATCTGCTGCTGCTCAACCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 903
Db 1522 ACTTCGGGAGATCTGCTGCTGCTCAACCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1581
Qy 904 CTTACTGCGGCTCTATTTCGCTGAGCGTGGACAACTTCAACGAGGTGCTGGAGGATGACC 963

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OM nucleic - nucleic search, using sw model

Run on: October 5, 2005, 20:34:43 ; Search time 788 Seconds
(without alignments)

10081.590 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 4: geneseqn2001as:*
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- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1335.6	99.5	1342	2	Az09482 Human Ih
2	1297	96.6	3372	4	Aah48729 Human HCN
3	1297	96.6	3372	13	Adg83419 Human tum
4	1295.4	96.5	3459	6	Aad29756 Human hyp
5	1194.4	89.0	1790	2	Aax84445 Human bra
6	1191.6	88.8	2125	10	Adc87558 Human GPC
7	1113.2	83.0	3431	4	Aah98302 Human EST
8	1048.6	78.1	3102	4	Aah48731 Murine HC
9	1032.4	76.9	1820	2	Aaz09488 Bovine re
10	992.4	73.9	2886	2	Aaz09491 Human Ih
11	927.2	69.1	4751	2	Aaz09496 Human hea
12	927.2	69.1	4751	6	Aad29757 Human hyp
13	927.2	69.1	5065	4	Aah48730 Human HCN
14	927.2	69.1	5065	13	Adr86593 Human HCN
15	927.2	69.1	5499	4	Aba09197 Human cat
16	871	64.9	1584	2	Aax84444 Mouse bra
17	753.4	56.1	3852	6	Aal44691 Human tra
18	753	56.1	2340	6	Abk86386 Human HCN
19	751.8	56.0	2217	8	Abx71090 Novel hum
20	751.8	56.0	2325	3	Aac66779 Human hyp

21	751.8	56.0	2325	8	Abz75841	Abz75841 Human HCN
22	751.8	56.0	2325	8	Abz58682	Abz58682 Human HCN
23	751.8	56.0	2325	8	ACA61916	ACA61916 cDNA enco
24	751.8	56.0	2325	10	ABX95515	ABX95515 cDNA enco
25	751.8	56.0	3496	6	AAD29758	Aad29758 Human hyp
26	751.8	56.0	3601	12	ADQ83229	Adq83229 Human tum
27	751.8	56.0	3601	13	ADQ85140	Adq85140 Human tum
28	751.4	56.0	2340	6	ABK86387	Abk86387 Human HCN
29	751.4	56.0	2340	6	ABK86385	Abk86385 Human HCN
30	735.2	54.8	2733	2	AAX84442	Aax84442 Mouse bra
31	720.8	53.7	3112	2	AZ09483	Aaz09483 Rat olfac
32	688.8	51.3	1507	2	AAX84446	Aax84446 Mouse bra
33	681.8	50.8	2990	10	ADJ95123	Adj95123 Novel NOV
34	680.2	50.7	1873	6	AAS18224	Aas18224 Human PCR
35	680.2	50.7	1873	6	AAS18223	Aas18223 Human PCR
36	680.2	50.7	2263	2	AAX84443	Aax84443 Human bra
37	680.2	50.7	2670	6	AAD29755	Aad29755 Human hyp
38	680.2	50.7	2673	8	ABZ75836	Abz75836 Human HCN
39	680.2	50.7	2673	8	ABZ58677	Abz58677 Human HCN
40	680.2	50.7	2673	8	ACA61911	ACA61911 cDNA enco
41	680.2	50.7	2673	10	ABX95510	Abx95510 cDNA enco
42	680.2	50.7	2748	6	ABT09623	Abt09623 Human HCN
43	680.2	50.7	2748	6	ABT09624	Abt09624 Human HCN
44	680.2	50.7	2748	6	ABT09630	Abt09630 Human HCN
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ALIGNMENTS

RESULT 1

AZ09482

ID AAZ09482 standard; DNA; 1342 BP.

XX AAZ09482;

AC AAZ09482;

XX 02-NOV-1999 (first entry)

DT Human Ih ion channel DNA fragment.

DE Human Ih ion channel DNA fragment.

XX Ih ion channel; human; sea urchin; fruit fly; rat; bovine; analgesic;

KW cardioactive; pacemaker; cardiac muscle; ion channel modulator;

KW treatment; diagnosis; ion channel-related disease; cardiac disease;

KW circulatory disorder; sinus ganglion regulation; sleep disorder;

KW cortico-thalamic neuron; pain; detection; mutation; ss.

XX Homo sapiens.

XX WO9942574-A1.

XX 26-AUG-1999.

XX 12-FEB-1999; 99WO-EP000942.

XX 17-FEB-1998; 98DE-01006581.

XX (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.

XX Baumann A, Boenigk W, Gause R, Scholten A, Seifert R, Kaupp B;

XX WPI; 1999-527472/44.

XX New nucleic acid encoding an Ih ion channel, used to identify specific

PT modulators, and for treatment, prevention and diagnosis of e.g. cardiac

PT disease.

PT Claim 3; Page 57; 82pp: German.

XX This invention describes a novel Ih ion channel, isolated from human, sea

CC urchin, bovine, rat, and fruitfly. The ion channels of the invention have

CC analgesic and cardioactive activity. The Ih ion channel participates in

CC the pacemaker function in cardiac muscle. The Ih ion channel nucleic acid

CC and its encoding protein is used to identify substances (A) that modulate

CC activity of ion channels; to treat and/or diagnose ion channel-related
CC diseases, particularly cardiac or circulatory disorders and to prevent
CC and/or treat cardiac/circulatory disorders (especially faulty regulation
CC of the sinus ganglion), sleep disorders (particularly abnormal function
CC of cortico-thalamic neurons) and/or pain. Fragments of the Ih ion channel
CC nucleic acid are used to detect mutations e.g. for differential
CC diagnosis. This sequence encodes a human Ih channel fragment isolated
CC from human thalamus tissue
XX

SQ Sequence 1342 BP; 252 A; 451 C; 390 G; 240 T; 0 U; 9 Other;

Query Match 99.5%; Score 1335.6; DB 2; Length 1342;
Best Local Similarity 100.0%; Pred. No. 3.4e-229;
Matches 1342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 GCTACATCATCTAGTGGAGGAGATCTTCACATGACCTATGACCTGGCCAGCGGTGA 120
QY 121 TGAGGATCTGCAATCTCATCAGCATGATCTGCTCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 121 TGAGGATCTGCAATCTCATCAGCATGATCTGCTCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 181 AGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
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DB 241 TGGTGAACCACTGCTGGAGTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 301 TGTCTGTGATCGGGTACGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
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QY 661 TGCGCAACCGGAGGAGATCGTCAATCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 661 TGCGCAACCGGAGGAGATCGTCAATCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
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DB 781 AGCACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
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DB 841 CCTACTTCGGGGAGATCTGCTGCTCACTCCCGGGCGCGCACCGGAGCGTGGCGGTG 900
QY 901 ACACCTACTGCGGCTCTTATTGCTGAGCGTGGACAACCTTCAACGAGGTGCTGGAGAGT 960
DB 901 ACACCTACTGCGGCTCTTATTGCTGAGCGTGGACAACCTTCAACGAGGTGCTGGAGAGT 960
QY 961 ACCCCATCATGCGGCGGCTTCCGAGAGCGTGGCCATCGACCGCTTGGACCCATCGGCA 1020
DB 961 ACCCCATCATGCGGCGGCTTCCGAGAGCGTGGCCATCGACCGCTTGGACCCATCGGCA 1020
QY 1021 AGAAGATTTCCATCTCTCTGCAAGGTGCGAGCATGACCTCAACTCGGGCGTATTCAACA 1080
DB 1021 AGAAGATTTCCATCTCTCTGCAAGGTGCGAGCATGACCTCAACTCGGGCGTATTCAACA 1080
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QY 1141 CCGAGCTGGGCTCAGCGGCTGGGCTCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
DB 1141 CCGAGCTGGGCTCAGCGGCTGGGCTCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
QY 1201 CGGCATCGCCACGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260
DB 1201 CGGCATCGCCACGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260
QY 1261 GCTCGTGGGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCG 1320
DB 1261 GCTCGTGGGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCG 1320
QY 1321 CGCACTGCHGCCNCTCACCC 1342
DB 1321 CGCACTGCHGCCNCTCACCC 1342

RESULT 2

AAH48729
ID AAH48729 standard; cdna; 3372 BP.
XX
AC AAH48729;
XX
DT 26-OCT-2001 (first entry)
XX
DE Human HCN2 cdna.
XX
KW Human; activator; patch-clamp; high through-put screening; inhibitor;
KW hyperpolarization-activated cation channel; HCN2; ss.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 36..2705
FT /*tag= a
FT /product= "HCN2"
XX
PN WO200159153-A2.
XX
PD 16-AUG-2001.
XX
PF 24-JAN-2001; 2001WO-EP000755.
XX
PR 12-FEB-2000; 2000DE-01006309.
XX
PA (AVET) AVENTIS PHARMA DEUT GMBH.
XX
PI Jansen H, Brueggemann A, Heitsch H, Goegelstein H;
XX
DR WPI; 2001-550023/61.
DR P-PSDB; AAB86461.
PT Identifying substances which modify activity of hyperpolarization-
PT activated cation channels using fluorescent imaging is useful to identify
PT possible therapeutic pharmaceuticals.

XX PS Disclosure; Page 38-39; 58pp; German.

XX CC This invention describes a novel method for identifying substances which

CC modify activity of hyperpolarization-activated cation channels (HACC), by

CC placing cells which express an HACC in an iso-osmotic sodium ion-free

CC buffer in the presence of a potential-sensitive fluorescent dye, and

CC measuring membrane potential after the addition of sodium ions. The

CC invention is used to identify activators or inhibitors of HACCs. Unlike

CC prior art patch-clamp techniques, this invention can be automated, and

CC allows high throughput put screening. This sequence encodes the human

CC hyperpolarization-activated cation channel protein HCN2 which is

CC described in the method of the invention

XX SQ Sequence 3372 BP; 515 A; 1304 C; 1076 G; 477 T; 0 U; 0 Other;

Query Match 96.6%; Score 1297; DB 4; Length 3372;

Best Local Similarity 99.0%; Pred. No. 2.8e-222;

Matches 1328; Conservative 7; Mismatches 3; Indels 3; Gaps 3;

QY 4 TGGGCTTCCACCAAGATCTCAGCCTCTCGGGCTGCTGGCGCTCTCAGCGCTCATCGCT 63

DB 1012 TGGGCTTCCACCAAGATCTCAGCCTCTCGGGCTGCTGGCGCTCTCAGCGCTCATCGCT 1071

QY 64 ACATCCATCAGTGGAGAGATCTTCCACATGACCTATGACCTGGCGCGCGGTGATGA 123

DB 1072 ACATCCATCAGTGGAGAGATCTTCCACATGACCTATGACCTGGCGCGCGGTGATGA 1131

QY 124 GGATCTGCAATCTCATCAGCATGATGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 183

DB 1132 GGATCTGCAATCTCATCAGCATGATGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1191

QY 184 TCCTGGTGGCCATGCTGAGGAATTCCTCCGGCGCACTGCTGGGTGCTCAATGGCATGG 243

DB 1192 TCCTGGTGGCCATGCTGAGGAATTCCTCCGGCGCACTGCTGGGTGCTCAATGGCATGG 1251

QY 244 TGAACCACTCGTGAGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 303

DB 1252 TGAACCACTCGTGAGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1311

QY 304 TGTGCTATCGGATACGGCG 363

DB 1312 TGTGCTATCGGATACGGCG 1371

QY 364 TCAGCATGATGTTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 423

DB 1372 TCAGCATGATGTTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1431

QY 424 TCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 483

DB 1432 TCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1491

QY 484 ACATGCTCTTCCCAAGCTGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 543

DB 1492 ACATGCTCTTCCCAAGCTGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1551

QY 544 ACCGTTACCGGGAAGATGTTTGAAGGAGCAGCATCTTGGCGAGCTCAACGGGCGCC 603

DB 1552 ACCGTTACCGGGAAGATGTTTGAAGGAGCAGCATCTTGGCGAGCTCAACGGGCGCC 1611

QY 604 TGGCGGAGGATCGTCAACTTCAACTGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 663

DB 1612 TGGCGGAGGATCGTCAACTTCAACTGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1671

QY 664 CCAAGCGGACCCCAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723

DB 1672 CCAAGCGGACCCCAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1731

QY 724 AGCGGGGTGATATCATCATCTCCGGAGAGGACCATCTGGGAGAGATGATGATCTTCCAGC 783

DB 1732 AGCGGGGTGATATCATCATCTCCGGAGAGGACCATCTGGGAGAGATGATGATCTTCCAGC 1791

QY 784 ACGGCGTGGTCAAGCTGCTCACTAAGGGCAAGGAGATGAGCTGCTCCGATGCTGCTCT 843

DB 1792 ACGGCGTGGTCAAGCTGCTCACTAAGGGCAAGGAGATGAGCTGCTCCGATGGCTCT 1851

QY 844 ACTTCGGGAGATCTGCTGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 903

DB 1852 ACTTCGGGAGATCTGCTGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1911

QY 904 CCTACTGCGCGCTCTATTGCTGAGCTGAGTGAACAATTCACAGAGTCTGGAGGATACC 963

DB 1912 CCTACTGCGCGCTCTATTGCTGAGCTGAGTGAACAATTCACAGAGTCTGGAGGATACC 1971

QY 964 CCATGATGCGGCGCGCTTTCGAGAGCGGTGGCCATCGACCGCTGACCGCATCGGCAAGA 1023

DB 1972 CCATGATGCGGCGCGCTTTCGAGAGCGGTGGCCATCGACCGCTTGGACCGCATCGGCAAGA 2031

QY 1024 AGAATTCATCTCTCTGCAACAAGGTGACGATGACCTCAACTCGGCGGTATTCAACAACC 1083

DB 2032 AGAATTCATCTCTCTGCAACAAGGTGACGATGACCTCAACTCGGCGGTATTCAACAACC 2091

QY 1084 AGGAGAACCCCATCATCCAGGAGATGCTCAAGTACGACCGCGAGATGGTGACAGGCGG 1143

DB 2092 AGGAGAACCCCATCATCCAGGAGATGCTCAAGTACGACCGCGAGATGGTGACAGGCGG 2151

QY 1144 AGCTGGGCTCAGGGCTGGGCTCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1202

DB 2152 AGCTGGG-TCAGCGCGTGGGCTCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2210

QY 1203 GCATCGCCACGCTGCGAGCGCGCGCGCATGAGCTTCTGCGCGCA-GTGGCGCGCGCG 1261

DB 2211 GCATCGCCACGCTGCGAGCGCGCGCGCATGAGCTTCTGCGCGCAAGTGGCGCGCG 2270

QY 1262 CTCGTGGGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 1321

DB 2271 CTCGTGGGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 2330

QY 1322 GCACCTGCHGCCNCTCACCC 1342

DB 2331 GCACCTGCHGCCNCTCACCC 2351

RESULT 3

ADQ83419

ID ADQ83419 standard; cDNA; 3372 BP.

XX

AC ADQ83419;

XX

XX 07-OCT-2004 (first entry)

DT

XX Human tumour-associated antigenic target (TAT) cDNA sequence #233.

DE human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;

XX cancer; cell proliferative disorder; gene; ss.

XX Homo sapiens.

OS

XX WO2004060270-A2.

XX

XX 22-JUL-2004.

PD

XX 15-OCT-2003; 2003WO-US029126.

PF

XX 18-OCT-2002; 2002US-041898P.

PR

XX (GETH) GENENTECH INC.

PA (WUTD//) WU T D.

PA (ZHOU//) ZHOU Y.

XX

XX Wu TD, Zhou Y;

PI

XX WPT; 2004-534300/51.

DR

XX New nucleic acid molecule and encoded polypeptide, for diagnosing,

XX preventing or treating cell proliferative disorders such as cancer.

PT

XX Claim 1; SEQ ID NO 233; 5504pp; English.

PS The present invention describes an isolated tumour-associated antigenic

XX target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide

CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of

CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%

CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-

CC (c). Also described: (1) an expression vector comprising the above

CC nucleic acid; (2) a host cell comprising the above expression vector; (3)

CC a process for producing a polypeptide; (4) an isolated polypeptide

CC comprising: (a) an amino acid sequence encoded by any of the above

CC nucleotide sequences; (b) an amino acid sequence encoded by the full-

CC length coding region of the above nucleotide sequences; or (c) a sequence

CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide

CC comprising the above polypeptide fused to a heterologous polypeptide; (6)

CC an isolated antibody that binds to the above polypeptide; (7) a process

CC for producing the antibody; (8) an isolated oligopeptide that binds to

CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)

CC binding organic molecule that binds to the above polypeptide; (10) a

CC composition of matter comprising the above (chimeric) polypeptide,

CC antibody, oligopeptide or TAT binding organic molecule, in combination

CC with a carrier; (11) an article of manufacture comprising a container and

CC the composition of matter contained within the container; (12) methods of

CC inhibiting the growth of a cell that expresses the above protein, where

CC the growth of the cell is at least in part dependent upon a growth

CC potentiating effect of the above protein; (13) a method of

CC therapeutically treating a mammal having a cancerous tumour comprising

CC cells that express the above protein; (14) a method of determining the

CC presence of a protein in a sample suspected of containing the protein

CC described above; (15) methods of diagnosing the presence of a tumour in a

CC mammal; (16) a method for treating or preventing a cell proliferative

CC disorder associated with increased expression or activity of the above

CC protein; and (17) a method of binding an antibody, oligopeptide or

CC organic molecule to a cell that expresses the protein described above.

CC The TAT sequences have cytostatic activities, and can be used in gene

CC therapy. The composition and methods are useful for diagnosing,

CC preventing or treating cancer. The composition is also used for preparing

CC a medicament for the therapeutic treatment or diagnostic detection of a

CC cell proliferative disorder or cancer. The present sequence represents a

XX human TAT cDNA sequence from the present invention.

SQ Sequence 3372 BP; 512 A; 1305 C; 1078 G; 477 T; 0 U; 0 Other;

Query Match 96.6%; Score 1297; DB 13; Length 3372;

Best Local Similarity 99.0%; Pred. No. 2.8e-222;

Matches 1328; Conservative 7; Mismatches 3; Indels 3; Gaps 3;

QY 4 TGGGCTTACCAAGATCCTCAGCCTCTCGGGCTGCTGGGCTCTCACGCCCTGATCCGCT 63

DB 1012 TGGGCTTACCAAGATCCTCAGCCTCTCGGGCTGCTGGGCTCTCACGCCCTGATCCGCT 1071

QY 64 ACATCCATCAGTGGGAGGAGATCTCCACATGACCTATGACCTGGCCAGCGGGTATGA 123

DB 1072 ACATCCATCAGTGGGAGGAGATCTCCACATGACCTATGACCTGGCCAGCGGGTATGA 1131

QY 124 GGATCTGCAATCTCATCAGCATGATCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 183

DB 1132 GGATCTGCAATCTCATCAGCATGATCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1191

QY 184 TCTGCT 243

DB 1192 TCTGCT 1251

QY 244 TGAACCACTCGTGGAGTGAATCTACTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 303

DB 1252 TGAACCACTCGTGGAGTGAATCTACTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1311

QY 304 TGTGATTCGGGTACGCGCGGCGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 363

DB 1312 TGTGATTCGGGTACGCGCGGCGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1371

QY 364 TCAGCATGATTGGGGTGCCACCTGCTACGCCATGTTTCATCGGCCACGCCACTGCGCTCA 423

1372	TCAGCATGATTGGGTGCCACCTGCTAGCCATGTTTCATCGGCCACGCCACTGCGCTCA	1431
424	TCCAGTCTCGTGAATCTCTCGGGGCCAGTACACAGGAGAGTACACAGAGTGGAGCAGT	483
1432	TCCAGTCTCGTGAATCTCTCGGGGCCAGTACACAGGAGAGTACACAGAGTGGAGCAGT	1491
484	ACATGCTCTCCACAGCTGTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	543
1492	ACATGCTCTCCACAGCTGTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1551
544	ACCGTTTACAGGGCAAGATGTTTGAACAGGACAGCATCTCGGGGAGCTCAACCGGCCCC	603
1552	ACCGTTTACAGGGCAAGATGTTTGAACAGGACAGCATCTCGGGGAGCTCAACCGGCCCC	1611
604	TGCGGGAGAGATGCTCAACTTCAACTCGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	663
1612	TGCGGGAGAGATGCTCAACTTCAACTCGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1671
664	CCACGGCGACCCCAACTTCTGTCAGGGCATGCTGACCAAGCTCAAGTTTCAGAGTCTTCC	723
1672	CCACGGCGACCCCAACTTCTGTCAGGGCATGCTGACCAAGCTCAAGTTTCAGAGTCTTCC	1731
724	AGCCGGGTGACTACATCATCTCCGCGAAGCCATCCGGAAGAGATGTAATTCATCCAGC	783
1732	AGCCGGGTGACTACATCATCTCCGCGAAGCCATCCGGAAGAGATGTAATTCATCCAGC	1791
784	ACGGGCTGCTAGCGTGTCTCAATAGGCAACAGGAGATGAAGTGTCCAGTGTCTCT	843
1792	ACGGGCTGCTAGCGTGTCTCAATAGGCAACAGGAGATGAAGTGTCTCCAGTGTCTCT	1851
844	ACTTCGGGAGATCTGCTGCTCTCACCCGGGGCGCGCACGCGAGCTGCGGGCTGACA	903
1852	ACTTCGGGAGATCTGCTGCTCTCACCCGGGGCGCGCACGCGAGCTGCGGGCTGACA	1911
904	CCTACTGCGGCTCTTATTCGCTGAGCGTGGAGCACTTCAACAGAGTGTGGAGGAGTACC	963
1912	CCTACTGCGGCTCTTATTCGCTGAGCGTGGAGCACTTCAACAGAGTGTGGAGGAGTACC	1971
964	CCATGATCGGGCGGCTCTCGAGAGCGTGGCCATCGACGCGCTGAGCGCATCGGCAAGA	1023
1972	CCATGATCGGGCGGCTCTCGAGAGCGTGGCCATCGACGCGCTGAGCGCATCGGCAAGA	2031
1024	AGATTTCATCTCTCTGACCAAGTGCAGCATGACCTCAACTCGGGCGTATTCAACAACC	1083
2032	AGATTTCATCTCTCTGACCAAGTGCAGCATGACCTCAACTCGGGCGTATTCAACAACC	2091
1084	AGGAAACGCCCATCATCCAGGAGATCGTCAAGTACGCCGAGATGGTGCAGCAGGCGG	1143
2092	AGGAAACGCCCATCATCCAGGAGATCGTCAAGTACGCCGAGATGGTGCAGCAGGCGG	2151
1144	AGTGGGCTCAGCGGCTGGGCTCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	1202
2152	AGTGGG-TCAGCGGCTGGGCTCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	2210
1203	GCCATCGCCAGCTGCAGCAGCGCGCGCGCATGAGCTTCTGCGCGGCA-GTGCGCGCGCG	1261
2211	GCCATCGCCAGCTGCAGCAGCGCGCGCATGAGCTTCTGCGCGGCA-GTGCGCGCGCG	2270
1262	CTGCTGGGCGCGCTGGGCTGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1321
2271	CTGCTGGGCGCGCTGGGCTGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2330
1322	GCACCTGCHGCNCTCACCC	1342
2331	GCACCTGCHGCNCTCACCC	2351

RESULT 4
AAD29756
ID AAD29756 standard; DNA; 3459 BP.
XX
AC AAD29756;

XX 17-MAY-2002 (first entry)
DT Human hyperpolarisation-activated cyclic nucleotide-gated channel 2 DNA.
DE Human: hyperpolarisation-activated cyclic nucleotide-gated channel; HCN;
XX therapy; stroke; ischaemia; head injury; epilepsy; Alzheimer's disease;
KW Parkinson's disease; learning disorder; memory; attention disorder; pain;
KW gut disorder; irritable bowel syndrome; IBS; sleep disorder; nootropic;
KW neuroprotective; cerbroprotective; antiinflammatory; anticonvulsant;
KW tranquiliser; vasotropic; ds.
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 54..2723
FT CDS /*tag= a
FT /product= "Human HCN2 protein"
XX
PN WO200202630-A2.
XX
XX 10-JAN-2002.
XX
XX 03-JUL-2001; 2001WO-GB002959.
XX
XX 03-JUL-2000; 2000GB-00016360.
XX 03-NOV-2000; 2000GB-00026946.
XX (SMIK) SMITHKLINE BEECHAM PLC.
XX
XX Strijbos PJLM, Bates S, Gloger I, Davies C;
PI
XX WPI; 2002-188422/24.
XX P-PSDB; AAE18676.
XX
XX New HCN channel polypeptides and polynucleotides which encode the
PT polypeptides, for the manufacture of compositions to treat stroke,
PT ischaemia, head injury, epilepsy, Alzheimer's disease, Parkinson's
XX disease.
XX
XX Claim 7; Page 52-53; 68pp; English.
XX
XX The invention relates to new uses of human hyperpolarisation-activated,
CC cyclic nucleotide-gated (HCN) channel polypeptides and their
CC polynucleotides. The HCN channel polypeptides and polynucleotides can be
CC used in the manufacture of medicaments to treat stroke, ischaemia, head
CC injury, epilepsy, Alzheimer's disease, Parkinson's disease, learning or
CC memory and attention disorders. These compounds may also be used in
CC treating pain, gut disorders, in particular Irritable bowel syndrome
CC (IBS) or sleep disorders. HCN polynucleotides and polypeptides may also
CC be employed as diagnostic reagents for detection of mutations in the
CC above stated diseases. The present sequence is human HCN2 channel DNA
XX
SQ Sequence 3459 BP; 569 A; 1317 C; 1094 G; 479 T; 0 U; 0 Other;
Query Match 96.5%; Score 1295.4; DB 6; Length 3459;
Best Local Similarity 99.0%; Pred. No. 5.4e-222;
Matches 1327; Conservative 7; Mismatches 4; Indels 3; Gaps 3;
QY 4 TGGCGCTTCAACAGATCCTAGCGCTCTCGCGGCTGCTCGCGCTCTCACGCGCTGATCCGCT 63
DB 1030 TGGCGCTTCAACAGATCCTAGCGCTCTCGCGGCTGCTCGCGCTCTCACGCGCTGATCCGCT 1089
QY 64 ACATCCATCACTGGAGAGATCTTCCACATGACCTATGACCTGGCGAGCGCGGTGATGA 123
DB 1090 ACATCCATCACTGGAGAGATCTTCCACATGACCTATGACCTGGCGAGCGCGGTGATGA 1149
QY 124 GGATCTGCAATCTCATGAGCATGATGCTGCTCTGCGCTGCGACTGGAGCGGCTGCTGCAGT 183
DB 1150 GGATCTGCAATCTCATGAGCATGATGCTGCTCTGCGCTGCGACTGGAGCGGCTGCTGCAGT 1209
QY 184 TCCTGGTGGCCATGCTGAGGACTTCCCGCGCAACTGCTGGGTGCTCAATGGCATGG 243

DB 1210 TCCTGGTGGCTATGCTGCAGGACTTCCCGCGCAACTGCTGGGTGCTCCATCAATGGCATGG 1269
QY 244 TGAACCACTCGTGGAGTGAACCTGTACTCTTCGCACTCTTCAAGGCCATGAGCCACATGC 303
DB 1270 TGAACCACTCGTGGAGTGAACCTGTACTCTTCGCACTCTTCAAGGCCATGAGCCACATGC 1329
QY 304 TGTGATCGGGTACCGCGCGGAGGCGCGGAGAGATGACGACATCTGGCTGACCATGC 363
DB 1330 TGTGATCGGGTACCGCGCGGAGGCGCGGAGAGATGACGACATCTGGCTGACCATGC 1389
QY 364 TCAGCATGATTTGGGTGCCACTCTGCTAGCCATGTTTCATCGCCACGCACTGCCCCTCA 423
DB 1390 TCAGCATGATTTGGGTGCCACTCTGCTAGCCATGTTTCATCGCCACGCACTGCCCCTCA 1449
QY 424 TCAGTTCGCTGACTCTTCGCGGCGCAGTACAGGAGAAGTACAAGAGGTGGAGAGT 483
DB 1450 TCAGTTCGCTGACTCTTCGCGGCGCAGTACAGGAGAAGTACAAGAGGTGGAGAGT 1509
QY 484 ACATGTCCTTCCACAAGCTGCCAGTACTTCCGCCAGAAGATCCAGCACTACTATGAGC 543
DB 1510 ACATGTCCTTCCACAAGCTGCCAGTACTTCCGCCAGAAGATCCAGCACTACTATGAGC 1569
QY 544 ACCGTTACCAGGCGAAGATGTTTGGAGGAGCAGCATCTGGCGGAGCTCAACGGGCCCC 603
DB 1570 ACCGTTACCAGGCGAAGATGTTTGGAGGAGCAGCATCTGGCGGAGCTCAACGGGCCCC 1629
QY 604 TGGCGGAGGAGATCGTCAACTTCAACTGCGGGAAGCTGGTGGCTCCATGCCCTGTTCG 663
DB 1630 TGGCGGAGGAGATCGTCAACTTCAACTGCGGGAAGCTGGTGGCTCCATGCCCTGTTCG 1689
QY 664 CCAAGCCGACCCCAACTTTCGTCACGCGCATGTCGACCAAGCTCAAGTTCGAGGTCTTCC 723
DB 1690 CCAAGCCGACCCCAACTTTCGTCACGCGCATGTCGACCAAGCTCAAGTTCGAGGTCTTCC 1749
QY 724 AGCGGGTGTACTACATCATCTCGGAGGAGCACCATCGGAGAGAGATGTACTTCATCCAGC 783
DB 1750 AGCGGGTGTACTACATCATCTCGGAGGAGCACCATCGGAGAGAGATGTACTTCATCCAGC 1809
QY 784 AGCGGGTGTACTACATCATCTCGGAGGAGCACCATCGGAGAGATGTACTTCATCCAGC 843
DB 1810 AGCGGGTGTACTACATCATCTCGGAGGAGCACCATCGGAGAGATGTACTTCATCCAGC 1869
QY 844 ACTTCGGGAGATCTCGCTGCTCACTCCGCGGCGCGCGCAGCGGAGGTGCGGGCTGACA 903
DB 1870 ACTTCGGGAGATCTCGCTGCTCACTCCGCGGCGCGCGCAGCGGAGGTGCGGGCTGACA 1929
QY 904 CCTACTCGCGCTCTATTTCGCTGAGGTGAGCAACTTCAACGAGGTGCTCGAGGAGTACC 963
DB 1930 CCTACTCGCGCTCTATTTCGCTGAGGTGAGCAACTTCAACGAGGTGCTCGAGGAGTACC 1989
QY 964 CCATGATGCGGCGCGCTTCGAGACGCTGGCCATCGACCGCTCGGACCGCATCGGCAAGA 1023
DB 1990 CCATGATGCGGCGCGCTTCGAGACGCTGGCCATCGACCGCTCGGACCGCATCGGCAAGA 2049
QY 1024 AGAATTCATCTCTTCGCAACAGGTGAGCATGACCTCAACTCGGGGTATTCACAAACC 1083
DB 2050 AGAATTCATCTCTTCGCAACAGGTGAGCATGACCTCAACTCGGGGTATTCACAAACC 2109
QY 1084 AGAGAAAGCCATCTCCAGGAGATGCTCAAGTACGACCGGAGATGCTGAGCAGGAGCGG 1143
DB 2110 AGAGAAAGCCATCTCCAGGAGATGCTCAAGTACGACCGGAGATGCTGAGCAGGAGCGG 2169
QY 1144 AGCTGGGCTCAGCGCGTGGGCTCTTCCCGCGCGCGCGCGCGCGCGCA-GTCACTCG 1202
DB 2170 AGCTGGG-TGAGCGGTGGGCTCTTCCCGCGCGCGCGCGCGCGCGCGCGAGTCACTCG 2228
QY 1203 GCCATGCCCACTGACAGCAGGCGGCGCATGAGCTTCTGCGCGCA-GTGGCGCGGCGG 1261
DB 2229 GCCATGCCCACTGACAGCAGGCGGCGCATGAGCTTCTGCGCGCGAGTGGCGCGGCGG 2288
QY 1262 CTGCTGGGCGCGCTGGGCTCGGCTCGCGGCTCGTGGCGCHGCHGCHGCHGCHGCHGCHG 1321
DB 2289 CTGCTGGGCGCGCTGGGCTCGGCTCGCGGCTCGTGGCGCGCGCGCGCGCGCGCGCGG 2348

Db 1619 AGGAGAACCCATCATCCAGGAGATCGTCAAAGTACGACCGCGAGATGCTGCACGAGCCG 1678
QY 1144 AGCTGGCTCAGCGCTGGGCTCTTCCGCGCGCGCGCGCGCGCA-GTCACTCG 1202
Db 1679 AGCTGGG-TAGGCGCTGGGCTTTTCCGCGCGCGCGCGCGCGCGCGGAGTCACTTCG 1737
QY 1203 GCCATGCCACGCTGAGCAGCGCGCGCGCGCATGAGCTTCTGCCCGCAG 1250
Db 1738 GCCATGCCACGCTGAGCAGCGCGCGCGCATGAGCTTCTGCCCGCAG 1785

RESULT 6
ADC87558
ID ADC87558 standard; DNA; 2125 BP.
XX
AC ADC87558;
XX
DT 01-JAN-2004 (first entry)
XX Human GPCR gene SEQ ID NO:2011.
DE
XX db; gene; human; GPCR;
KW guanosine triphosphate-binding protein coupled receptor; gene therapy.
XX Homo sapiens.
XX
XX BP1270724-A2.
XX
XX PD 02-JAN-2003.
XX
XX 18-JUN-2002; 2002BP-00013517.
XX
XX PR 18-JUN-2001; 2001JP-00246789.
XX
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX
XX Suwa M, Asai K, Akiyama Y, Aburatani H;
XX WPI; 2003-315783/31.
XX P-PSDB; ADC87559.
XX
XX New polynucleotide, useful for preparing a composition for treating a
PT polynucleotide, useful for increased or suppressed activity or expression of the
PT guanosine triphosphate-binding protein coupled receptor.
XX
XX Claim 1; SEQ ID NO 2011; 28pp; English.
XX
XX The invention relates to a novel polynucleotide encoding a guanosine
CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
CC the invention may have a use in gene therapy. The polynucleotide and
CC polypeptide are useful for preparing a composition for treating a patient
CC in need of increased or suppressed activity or expression of the
CC guanosine triphosphate-binding protein coupled receptor. The
CC polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
CC invention.
XX
XX Sequence 2125 BP; 370 A; 721 C; 655 G; 379 T; 0 U; 0 Other;
SQ

Query Match 88.8%; Score 1191.6; DB 10; Length 2125;
Best Local Similarity 95.2%; Pred. No. 1.8e-203;
Matches 1276; Conservative 7; Mismatches 47; Indels 10; Gaps 5;

QY 4 TGGCTTCAACAAGATCCTCAGCCTCTCGGGCTGTGCGCTCTCAAGCTGATCGCT 63
Db 688 TGGCTTCAACAAGATCCTCAGCCTCTCGGGCTGTGCGCTCTCGGGCTGATCGCT 747
QY 64 ACATCCATCAGTGGAGAGATCTTCCATGACCTATGACCTGGCGCGCGGTATGA 123
Db 748 ACATCCACCACTGGAGGAGATCTTCCATGACCTATGACCTGGCGCGCGGTATGC 807
QY 124 GGATCTGCAATCTCATCAGATGATGCTGTGCTTCTGCCACTGGAGCGGTGCTGCAGT 183

Db 808 GGTCTGCAACCTCATCATAGTATGATGCTGTGCTCTGCGCATGGGATGGCTGCTGCAGT 867
QY 184 TCTGCTGCCCATCTGCTGAGGACTTCCCGCGCAACTGTCTGGGTGTCCATCAATGGCATCG 243
Db 868 TCTGCTGGCCATCTGCTGAGGACTTCCCGTGAACCTGTCTGGGTGTCCATCAATGGCATCG 927
QY 244 TGAAACAATCTGFGAGTGAATGTATCTCTTCCGCACTCTTCAAGGCGCATGAGCCATCG 303
Db 928 TGAAACAATCTGFGAGTGAATGTATCTCTTCCGCACTCTTCAAGGCGCATGAGCCATCG 987
QY 304 TGTGATCGGCTACGCGCGCGAGGCGCGGAGAGCATGACGACATCTGCGTGCACCATCG 363
Db 988 TGTGATCGGCTATGCGCGCGAGGCGCGGAGAGCATGACGACATCTGCGTGCACCATCG 1047
QY 364 TCAGCATGATTTGCTGGTGCACCTGCTACGCCATGTTTCATCGGCCACGCACTGCGCTCA 423
Db 1048 TCAGCATGATTTGCTGGTGCACCTGCTACGCCATGTTTCATCGGCCACGCACTGCGCTCA 1107
QY 424 TCCAGTCTGCTGCACTCTCGCGCGCCAGTACAGAGAGTACAGAGAGTGGAGCAGT 483
Db 1108 TCCAGTCTGCTGCACTCTCGCGCGCCAAATACC---AGAAGTACAGAGAGTGGAGCAGT 1164
QY 484 ACATGCTCTTCCAAAGCTGCGAGTCTCGCGCAGAGATCCACGACTACTATGAGC 543
Db 1165 ACATGCTCTTCCAAAGCTGCGCGCGCACTTCCGCGAGAGATCCACGACTACTACGAGC 1224
QY 544 ACCGTTACCAGGCGCAAGATGTTTGAGAGGACAGCATCTCGCGCGAGCTCAACGGGCCCC 603
Db 1225 ACCGTTACCAGGCGCAAGATGTTTGAGAGGACAGCATCTCGCGCGAGCTCAACGGGCCCC 1284
QY 604 TCGCGGAGGAGATCGTCAACTTCAACTGCGGAAAGCTGTGCTCCATCGCGCTGTTG 663
Db 1285 TCGCGGAGGAGATGTTCAACTTCAACTGCGGAAAGCTGTGCTCCATCGCGCTGTTG 1344
QY 664 CCAGCGCGACCCCACTTCTGTCAGCGCATCTGACCAAGCTCAAGTTCGAGGCTCTTC 723
Db 1345 CCAATGCTGACCCCACTTCTGTCAGCGCATCTGACCAAGCTCAAGTTCGAGGCTCTTC 1404
QY 724 AGCGGGTCACTACATCATCTCGGAGGACCATCGGAAAGATGTACTTTCATCCAGC 783
Db 1405 AGCGGGTCACTACATCTATCTCCGGAAGGACCATCGG---GAAGATGTACTTTCATCCAGC 1461
QY 784 AGCGGTGTCTGAGCGTGTCTACTAAGGGCAACAAGAGATGAAGTGTGCGATGGCTCTCT 843
Db 1462 AGCGGTGTCTGAGCGTGTCTGCTAAGGGCAACAAGAGATGAAGTGTTCGATGGCTCTCT 1521
QY 844 ACTTCGGGAGATCTGCTGCTCAACCGGGGCGCGCACGGGAGCGTGCAGGCTGACA 903
Db 1522 ACTTCGGAGAGATCTGCTGCTCAACCGGGGCGCGCACCGCATGCGAGCGTGCAGGCA 1581
QY 904 CCTACTGCGCGCTCTATTCGCTGAGGTGCGACAACCTTCAACGAGGTGCTGGAGAGTACC 963
Db 1582 CCTATTGCGCGCTCTTTCGCTGAGGTGCGACAACCTTCAACGAGGTGCTGGAGAGTACC 1641
QY 964 CCATGATGCGGGCGCGCTTTCGAGAGCGGTGGCCATCGACCGCTTGAACCGCATCGGCAAGA 1023
Db 1642 CCATGATGCGGGCGCGCTTTCGAGAGCGGTGGCCATCGACCGCTTGAACCGCATCGGCAAGA 1701
QY 1024 AGAATTCATCTCTGCGCAAGGTGCGAGCATGACCTCAACTCGGGCGGTATTCACACACC 1083
Db 1702 AGAATTCATCTCTCTGCGCAAGGTGCGAGCATGACCTTAACTCGGGCGGTATTCACACACC 1761
QY 1084 AGGAGAACGCCCATCATCCAGGAGATGCTCAAGTACGACCGCGAGATGTTGACAGCGCG 1143
Db 1762 AGTAGAACGCCCATCATCCAGGAGATGCTCAAGTACGACCGCGAGATGTTGACAGCGCG 1821
QY 1144 AGCTGGGCTCAGCGCTGGGCGCTCTTTCGCGCGCGCGCGCGCGCGCGAGTCACTTCGG 1203
Db 1822 AGCTGGG-TCAGGCGCTGGGCGCTCTTTCGCGCGCGCGCGCGCGCGAG--GTCACTTCGG 1878
QY 1204 CCATCGCCACGCTGACAGCGCGCGCGCATGAGCTTCTGCGCGCA-GTGGCGGCGCGC 1262
Db 1879 CCATCGCCACGCTGACAGCGCGCGTGTGTATGAGCTTCTGCGCGCGAGGTGCGCGCGCGC 1938

QY 1186 CCGCCGAGTCACTCGGCCATCGCACGCTGC----AGCAGCGCGGCCATGAGCTTTC 1241
|||||
DB 2229 CCGCCGAGGTCACTCGGGCAATCGCGAGCTGCGAGCAGCGCGGCCATGAGCTTTC 2288
|||||
QY 1242 TGCCCGCA-GTGGCGGCGCGCTCGTGGGCGCGCTGGCGCTCGCGCGCGCTCGTG 1300
|||||
DB 2289 TGCCCGAGGTGGCGGCGCGCTCGTGGGCGCGCTGGCGCTCGCGCGCGCTCGTG 2348
|||||
QY 1301 CGCHGCVNDYHCCGGGSGCGCACCTGCHGCNCCTCACCC 1342
|||||
DB 2349 CGCGCGCGCGCGCGCGCGCGCACCTGCGCGCGCGCTCACCC 2390
|||||

RESULT 8
AAH48731
ID AAH48731 standard; cDNA; 3102 BP.
XX
AC AAH48731;
XX
DT 26-OCT-2001 (first entry)
XX
XX Murine HCN2 cDNA.
XX
XX Murine; activator; patch-clamp; high through-put screening; inhibitor;
KW hyperpolarization-activated cation channel; HCN2; ss.
KW
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
FH 36..2627
FT /*tag= a
FT /product= "HCN2"
FT
XX
PN WO200159153-A2.
XX
XX 16-AUG-2001.
XX
XX 24-JAN-2001; 2001WO-EP000755.
XX
XX 12-FEB-2000; 2000DE-01006309.
XX
XX (AVET) AVENTIS PHARMA DEUT GMBH.
XX
XX Jansen H, Brueggemann A, Heitsch H, Goegelein H;
PI P-PSDB; AAB86463.
XX
XX WPI; 2001-550023/61.
XX
XX P-PSDB; AAB86463.
XX
PT Identifying substances which modify activity of hyperpolarization-
PT activated cation channels using fluorescent imaging is useful to identify
PT possible therapeutic pharmaceuticals.
XX
XX Disclosure; Page 49-50; 59pp; German.
XX
XX This invention describes a novel method for identifying substances which
XX modify activity of hyperpolarization-activated cation channels (HACC), by
XX placing cells which express an HACC in an iso-osmotic sodium ion-free
XX buffer in the presence of a potential-sensitive fluorescent dye, and
XX measuring membrane potential after the addition of sodium ions. The
XX invention is used to identify activators or inhibitors of HACCs. Unlike
XX prior art patch-clamp techniques, this invention can be automated, and
XX allows high through put screening. This sequence encodes the murine
XX hyperpolarization-activated cation channel protein HCN2 which is
XX described in the method of the invention
XX
SQ Sequence 3102 BP; 568 A; 1077 C; 935 G; 522 T; 0 U; 0 Other;
Query Match 78.1%; Score 1048.6; DB 4; Length 3102;
Best Local Similarity 87.6%; Pred. No. 6e-178;
Matches 1173; Conservative 6; Mismatches 156; Indels 4; Gaps 3;
4 TGCGTTCCCAAGATCTCAGCTCTCTGGCGTCTCGCGCTCTCAGCGTGTATCGCT 63
|||||

DB 931 TGCGTTCCCAAGATCTCAGCTCTCTGGCGTCTCTGGCGTATCATCGGCTCATCCGAT 990
QY 64 ACATCCATCAGTGGGAGAGATCTTCCACATGACCTATGACCTGGCGAGCGGGTGAATCA 123
|||||
DB 991 ATATCCACGAGTGGGAGAGATTTTCCACATGACCTAGACCTGGCAAGTGCAGTGATGC 1050
|||||
QY 124 GGATCTGCAATCTCATCAGCATGATGCTGCTCTGCACTGGGAGCGCTGCTGCACT 183
1051 GCATCTGTAACTGATCAGCATGATGCTCTCTGCACTGGGAGCGTTCGCTGCACT 1110
|||||
QY 184 TCTTGGTGGCCATGCTGAGGACTTCCCGCGCAACTGCTGGGTGTCTCAATGGCATGG 243
1111 TCTTGGTGGCCATGCTGCAAGACTTCCCGAGCGACTGCTGGGTGTCTCAATCAACATGG 1170
|||||
QY 244 TGAAACACTCGTGGAGTGAATGTACTTCTTCGCACTCTTCAAGGCCATGAGCCATGTC 303
1171 TGAAACACTCGTGGAGGAGCTCTACTGTTTCGCGCTCTTCAAGGCCATGAGCCATGTC 1230
DB 304 TGTGATCGGGTACGGCGCGGAGGCGCCGAGAGCATGAGGACATCTGGCTGACCATGC 363
1231 TGTGATCGGCTACGGCGCGGAGGCGCCGAGAGCATGAGGACATCTGGCTGACCATGC 1290
DB 364 TCAGCATGATTTGGGTGCCACTGCTACGCCATGTTTCATCGGCCACGCACTGCGCTCA 423
1291 TCAGCATGATTCGTAGCGCCACTGCTATGCCATGTTTCATGGGCAAGCATGCGCTCA 1350
424 TCCAGTTCGCTGCACTCTCGCGCGCCAGTACAGGAGAAAGTACAAAGAGGTGGAGCAGT 483
1351 TCAGTTCCTTGGATTCGTCACGGCGCCATACAGGAGAAAGTACAAAGAGGTAGAGCAAT 1410
484 ACATGTCTTCCCAAGTTCGCGCATGCTTCGCGCAGAAAGTCCAGCATCTATGAGC 543
1411 ACATGTCTTCCCAAGTTCGCGCATGCTTCGCGCAGAAAGTCCAGCATCTATGAGC 1470
544 ACCGTTACAGGCGCAAGATGTTTGACGAGCAGCATCTGGCGAGCTCAACGGGCCCC 603
1471 ACCGTTACAGGCGCAAGATGTTTGACGAGCAGCATCTGGCGAGCTCAACGGGCCCC 1530
604 TGCGGAGGAGATCGTCAACTTCACTGCGGAGGCTGGTGGCTCCATGCGCGCTGTTTCG 663
1531 TGCGTGGAGGATTTGAACTTCACTGCGGAGGCTGGTGGCTTCATGCGCGCTGTTTCG 1590
664 CCAACGCCGACCCCAACTTTCGTCACGGCCATGCTGACCAAGCTCAAGTTCGAGGTCTTCC 723
1591 CCAATGACAGCCCAACTTTCGTCACAGCCATGCTGACCAAGCTCAAAATTTGAGGTCTTCC 1650
724 AGCGGGGTGATATCATATCCCGGAAGGACCATCCGGAAGAGATGTTTTCATCCAGC 783
1651 AGCGGGGTGATATCATATCCCGGAAGGACCATCCGGAAGAGATGTTTTCATCCAGC 1710
784 AGCGGGGTGATATCATATCCCGGAAGGACCATCCGGAAGAGATGTTTTCATCCAGC 843
1711 ATGGGGTGGTGGAGTGTCTCACGAGGGGCAACGAGAGATGAAAGTGTGCGATGGCTCT 1770
844 ACTTTCGGGAGATTCCTGCTCTCACCGGGGCGCGCCAGCGAGCGTGGGGGTGACA 903
1771 ATTTTCGGGAGATTCCTGCTCTCACGAGGGCGCGCGTACCGGAGCGTGGAGCTGACA 1830
904 CTTACTCGCGCTCTATTCGCTGAGCGTGAGCAAACTTCAACGAGGTGCTTGGAGGAGTACC 963
1831 CTTACTCGCGCTCTATTCGCTGAGCGTGAGCAAACTTCAACGAGGTGCTTGGAGGAGTACC 1890
964 CCAATGATGGCGCGCTTTCGAGACGCTGGCCATCCAGCGCTTGGAGCGGATCGGCAAGA 1023
1891 CCAATGATGGCGCGCTTTCGAGACGCTGGCCATCCAGCGCTTGGAGCGGATCGGCAAGA 1950
1024 AGAATTCATCTCTGCAAGGTGAGCATGACCTCAACTCGGGCGTATTCAACAAC 1083
1951 AGAATTCATCTCTGCAAGGTGAGCATGATCTCAGCTCAGGTGTTGTTCAACAAC 2010
1084 AGGAGAACGCTATCCATCCAGGAGATGCTCAAGTACGACCGCGAGATGGTGCAGAGCCG 1143
2011 AGGAGAACGCTATCCATCCAGGAGATGCTCAAAATATGACCGGTGAGATGGTGCAGAGCAG 2070
DB

Db 1583 GAACCTCGATCTGTACACAGGTGTCAGCAGCACTCAACTCTGGCGTGTAAACACCA 1642
 QY 1085 GGAGAACCCATCATCCAGGAGATCGTCAAGTACGACCGGAGATGTGAGCAGGCGGA 1144
 Db 1643 GGAGAACCCATCATCCAGGAGATGTCAAGTATGACCGGAGATGTGAGCAGGCGTA 1702
 QY 1145 GCTGGGCTCAGCGGTGGGCTCTTCCGCGCGCGCGCGCGCGCGCA-GTCACTTCGG 1203
 Db 1703 GCTGGGC-CAGGTGTGGCTCTTCCGCGCACCGCGCACCTCCACAGGCGACCTCAG 1761
 QY 1204 CCATCGCCAGCTCAGCAGCGCGGCGCATGAGCTTCTGCGCGCA 1249
 Db 1762 CCATTGCCAGCTGCAGCA-GCCGTGGCCATGAGCTTCTGTCCACA 1806

RESULT 10

AAZ09491
 ID AAZ09491 standard; DNA; 2886 BP.

AC AAZ09491;

DT 02-NOV-1999 (first entry)

XX Human Ih ion channel DNA fragment #2.

XX Ih ion channel; human; sea urchin; fruit fly; rat; bovine; analgesic;
 KW cardioactive; pacemaker; cardiac muscle; ion channel modulator;
 KW treatment; diagnosis; ion channel-related disease; cardiac disease;
 KW circulatory disorder; sinus ganglion regulation; sleep disorder;
 KW cortico-thalamic neuron; pain; detection; mutation; ss.

XX Homo sapiens.

OS

XX WO9942574-A1.

XX 26-AUG-1999.

XX 12-FEB-1999; 99WO-EP000942.

XX 17-FEB-1998; 98DE-01006581.

XX (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.

XX Baumann A, Boenigk W, Gauss R, Scholten A, Seifert R, Kaupp B;

XX WPI; 1999-527472/44.

XX New nucleic acid encoding an Ih ion channel, used to identify specific
 PT modulators, and for treatment, prevention and diagnosis of e.g. cardiac
 PT disease.

XX Disclosure; Page 67-68; 82pp; German.

XX This invention describes a novel Ih ion channel, isolated from human, sea
 CC urchin, bovine, rat, and fruitfly. The ion channels of the invention have
 CC analgesic and cardioactive activity. The Ih ion channel participates in
 CC the pacemaker function in cardiac muscle. The Ih ion channel nucleic acid
 CC and its encoding protein is used to identify substances (A) that modulate
 CC activity of ion channels; to treat and/or diagnose ion channel-related
 CC diseases, particularly cardiac or circulatory disorders and to prevent
 CC and/or treat cardiac/circulatory disorders (especially faulty regulation
 CC of the sinus ganglion), sleep disorders (particularly abnormal function
 CC of cortico-thalamic neurons) and/or pain. Fragments of the Ih ion channel
 CC nucleic acid are used to detect mutations e.g. for differential
 CC diagnosis. This sequence encodes a human Ih channel fragment isolated
 CC from human thalamus tissue

XX Sequence 2886 BP; 605 A; 774 C; 940 G; 558 T; 0 U; 9 Other;

XX Query Match 73.9%; Score 992.4; DB 2; Length 2886;

XX Best Local Similarity 98.8%; Pred. No. 6.4e-168;

XX Matches 1007; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 4 TGGCGTTCACCAAGATTCCTCAGCCTCTGCGGCTGTGCGCTCTCAGCGCTGATCGGCT 63
 Db 521 TGGCGTTCACCAAGATTCCTCAGCCTCTGCGGCTGTGCGCTCTCAGCGCTGATCGGCT 580
 QY 64 ACATCCATCAGTGGGAGGAGATCTTCACATGACCTATGACCTGGGAGCGGCTGATGA 123
 Db 581 ACATCCATCAGTGGGAGGAGATCTTCACATGACCTATGACCTGGGAGCGGCTGATGA 640
 QY 124 GGATCTGCAATCTCATCAGCATGATGCTGCTCTGCGCACTGGGAGCGGCTGCTGAGT 183
 Db 641 GGATCTGCAATCTCATCAGCATGATGCTGCTCTGCGCACTGGGAGCGGCTGCTGAGT 700
 QY 184 TCCGTGTGCCATGCTGTCAGGACTTCCCGCGCAACTGCTGGGTGTTCATCAATGGCATGG 243
 Db 701 TCCGTGTGCCATGCTGTCAGGACTTCCCGCGCAACTGCTGGGTGTTCATCAATGGCATGG 760
 QY 244 TGAACCACTCGTGGAGTGAATGTACTCTTCGCACTCTTCAAGGCCATGAGCCATGTC 303
 Db 761 TGAACCACTCGTGGAGTGAATGTACTCTTCGCACTCTTCAAGGCCATGAGCCATGTC 820
 QY 304 TGTGCATCGGTACGCGCGGAGGCGCGGAGAGCATGACGAGCATCTGCTGACCATGC 363
 Db 821 TGTGCATCGGTACGCGCGGAGGCGCGGAGAGCATGACGAGCATCTGCTGACCATGC 880
 QY 364 TCAGCATGATTTGGGTGCCACTGCTACGCCATTTTCATCGGCCACGCCACTGCGCTCA 423
 Db 881 TCAGCATGATTTGGGTGCCACTGCTACGCCATTTTCATCGGCCACGCCACTGCGCTCA 940
 QY 424 TCCAGTGTGACTCTCTCGCGGCGCAGTACCGAGGAGATGATCAAGAGGTTGGAGCAGT 483
 Db 941 TCCAGTGTGACTCTCTCGCGGCGCAGTACCGAGGAGATGATCAAGAGGTTGGAGCAGT 1000
 QY 484 ACATGTCTTCCCAAGCTGCGCAGTGTCTTCGCGCAGAGATTCACAGCTACTATGAGC 543
 Db 1001 ACATGTCTTCCCAAGCTGCGCAGTGTCTTCGCGCAGAGATTCACAGCTACTATGAGC 1060
 QY 544 ACCGTTACAGGCGCAAGATGTTTTCAGGAGACAGCATCTTGGCGAGCTCAACGGGCCCC 603
 Db 1061 ACCGTTACAGGCGCAAGATGTTTTCAGGAGACAGCATCTTGGCGAGCTCAACGGGCCCC 1120
 QY 604 TGGCGGAGGAGATCGTCAACTTCACTGCGGAGAGCTGTGGCTTCAGTCCGCTGTTCG 663
 Db 1121 TGGCGGAGGAGATCGTCAACTTCACTGCGGAGAGCTGTGGCTTCAGTCCGCTGTTCG 1180
 QY 664 CCAACCGCGAGCCCCCACTTCGTCACGCGCATCTGACCAAGCTCAAGTTTCGAGGCTTTC 723
 Db 1181 CCAACCGCGAGCCCCCACTTCGTCACGCGCATCTGACCAAGCTCAAGTTTCGAGGCTTTC 1240
 QY 724 AGCGGGTGTACTACATCATCCGGAAGGACCATCCGGAAGAGATGTACTTTCATCCAGC 783
 Db 1241 AGCGGGTGTACTACATCATCCGGAAGGACCATCCGGAAGAGATGTACTTTCATCCAGC 1300
 QY 784 AGCGGGTGTACTACATCATCCGGAAGGACCATCCGGAAGAGATGTACTTTCATCCAGC 843
 Db 1301 AGCGGGTGTACTACATCATCCGGAAGGACCATCCGGAAGAGATGTACTTTCATCCAGC 1360
 QY 844 ACTTTCGGGAGATCTGCTGCTCAACCGGGCGCGCGCAGCGGAGCTGTCCGAGTGGCT 903
 Db 1361 ACTTTCGGGAGATCTGCTGCTCAACCGGGCGCGCGCAGCGGAGCTGTCCGAGTGGCT 1419
 QY 904 CCTACTCGCGCTCTTATTCGCTGAGCGTGGACAACTTCAACGAGGTTGCTGGAGAGTACC 963
 Db 1420 CCTACTCGCGCTCTTATTCGCTGAGCGTGGACAACTTCAACGAGTGTGGAGAGTACC 1479
 QY 964 CCATGATGCGGCGGCTTTCGAGACGGTGGCCATGACCGCTTGGAGCCGATCGGCAG 1022
 Db 1480 CCATGATGCGGCGGCTTTCGAGACGGTGGCCATGACCGCTTGGAGCCGATCGGTGAG 1538

RESULT 11

AAZ09496

ID AAZ09496 standard; DNA; 4751 BP.

XX

AAZ09496;
02-NOV-1999 (first entry)
Human heart tissue Ih ion channel DNA.
Ih ion channel; human; sea urchin; fruit fly; rat; bovine; analgesic;
cardioactive; pacemaker; cardiac muscle; ion channel modulator;
treatment; diagnosis; ion channel-related disease; cardiac disease;
circulatory disorder; sinus ganglion regulation; sleep disorder;
cortico-thalamic neuron; pain; detection; mutation; ss.
Homo sapiens.
W09942574-A1.
26-AUG-1999.
12-FEB-1999; 99WO-BP000942.
17-FEB-1998; 98DE-01006581.
(KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
Baumann A, Boenigk W, Gauss R, Scholten A, Seifert R, Kaupp B;
WPI; 1999-527472/44.
New nucleic acid encoding an Ih ion channel, used to identify specific
modulators, and for treatment, prevention and diagnosis of e.g. cardiac
disease.
Disclosure; Page 72-74; 82pp; German.
This invention describes a novel Ih ion channel, isolated from human, sea
urchin, bovine, rat, and fruitfly. The ion channels of the invention have
analgesic and cardioactive activity. The Ih ion channel participates in
the pacemaker function in cardiac muscle. The Ih ion channel nucleic acid
and its encoding protein is used to identify substances (A) that modulate
activity of ion channels; to treat and/or diagnose ion channel-related
diseases, particularly cardiac or circulatory disorders and to prevent
and/or treat cardiac/circulatory disorders (especially faulty regulation
of the sinus ganglion), sleep disorders (particularly abnormal function
of cortico-thalamic neurons) and/or pain. Fragments of the Ih ion channel
nucleic acid are used to detect mutations e.g. for differential
diagnosis. This sequence encodes a human Ih channel fragment isolated
from heart tissue
Sequence 4751 BP; 829 A; 1737 C; 1426 G; 759 T; 0 U; 0 Other;
Query Match 69.1%; Score 927.2; DB 2; Length 4751;
Best Local Similarity 84.7%; Pred. No. 2.9e-156;
Matches 1040; Conservative 0; Mismatches 188; Indels 0; Gaps 0;
4 TGGCGTTCCACGAGATCCTCAGCCTCTCGGGTGTGGCTCTCAGCGCTGATCCGCT 63
2126 TCGGCTTCAAGAGATCCCTAGCCTCTTACGCTGTGTACGCTCTCCCGCTCAATCGAT 2185
64 ACATCCATCAGTGGGAGGAGATCTCCACATGACCTATGACCTGGCGAGCGGTGATGA 123
2186 ATATTCCACAGTGGGAGAGATCTTCCATGACCTGACCTGGCGAGCGGTGTGC 2245
124 GGATCTGCAATCTCATCAGATGATGCTGCTGTGCACTTGGGAGCGGTGCTGCACT 183
2246 GCATCGTGAACCTCATCGGCATGATGCTGCTGTGCACTGGGAGCGGTGCTGCACT 2305
184 TCGTGTGCCATGCTGCGAGGATCTCCGGGCACTGCTGGGTTCATCAATGGCATGG 243
2306 TCGTGTACCAATGCTTACAGGATCTCCCTGACGACTGCTGGGTGTTCATCAACAACATGG 2365
244 TGAACCACTCGTGGAGTGAACCTGCTTCTGCACTCTTCAAGGCGCATGAGCCATGC 303
2366 TGNACAACTCCTGGGGAAGCAGTACTCTCTACGCGCTCTTCAAGGCCATGAGCCATGC 2425

QY 304 TGTGATCGGTACGGCGGCGAGAGCATGACGAGCATCTGGCTGACATGC 363
DB 2426 TGTGATCGGTACGGCGGCGAGGCGCGCTGGGCTCTGGCTCACAATGC 2485
QY 364 TCAGCATGATTGTGGTGCACCTGTACGCCATGTTTCATCGGCCACGCACTGCGCTCA 423
DB 2486 TCAGCATGATTGTGGTGCACCTGTACGCCATGTTTCATCGGCCACGCACTGCGCTCA 2545
QY 424 TCCAGTCTGCACTCTCGCGGCGCAGTACCAGGAGATGATCAAGAGGTGGAGCAGT 483
DB 2546 TCCAGTCTGCACTCTCGCGGCGCAGTACCAGGAGATGATCAAGAGGTGGAGCAGT 2605
QY 484 ACATGCTCTTCCAGAGCTGCGAGTTCGCGCAGAGATCCAGCACTACTATGAGC 543
DB 2606 ACATGCTCTTCCAGAGCTGCGCGCCGACACCCGCGAGCGCATCCAGCACTACTAGAGC 2665
QY 544 ACCGTTACAGGGCAAGATGTTTACGAGGAGCAGCATCTGGCGAGGTCAACGGGCCCC 603
DB 2666 ACCGTTACAGGGCAAGATGTTTACGAGGAGGAGCATCTGGCGAGGTCAACGGGCCCC 2725
QY 604 TGGGGAGGAGATCTCAACTTCAATGCGCGAAGCTGGTGGCTTCCATGCCGCTGTTGG 663
DB 2726 TGGGGAGGAGATCATCAACTTCAATGCGCGAAGCTGGTGGCTTCCATGCCGCTGTTGG 2785
QY 664 CCNAGCGCGACCCCAACTTCTGTCAGGCGCATGCTGACCAAGCTCAAGTTTCAGAGTCTTCC 723
DB 2786 CCNAGCGCGACCCCAACTTCTGTCAGGCGCATGCTGACCAAGCTCAAGTTTCAGAGTCTTCC 2845
QY 724 AGCGGGTGACTTACATCATCGCGAAGGACCATCGGGAAGAGATGACTTTCATCCAGC 783
DB 2846 AGCGGGTGACTTACATCATCGCGAAGGACCATCGGGAAGAGATGACTTTCATCCAGC 2905
QY 784 AGCGGGTGACTTACATCATCGCGAAGGACCATCGGGAAGAGATGACTTTCATCCAGC 843
DB 2906 AGCGGGTGACTTACATCATCGCGAAGGACCATCGGGAAGAGATGACTTTCATCCAGC 2965
QY 844 ACTTGGGAGATCTGCTGCTGCTCAGCGGCGCGCGCGAGCGCTGCGGCTGACA 903
DB 2966 ACTTGGGAGATCTGCTGCTGCTCAGCGGCGCGCGCGAGCGCTGCGGCTGACA 3025
QY 904 CCTACTGCGGCTCTATTTCGCTGAGCGTGGACAACTTCAACGAGGTGCTGGAGGAGTACC 963
DB 3026 CCTACTGCGGCTCTATTTCGCTGAGCGTGGACAACTTCAACGAGGTGCTGGAGGAGTACC 3085
QY 964 CCATGATCGGCGCGCTTTCGAGAGCGGTGGCGCATCGACCGCTGACCGCATCGGCAAGA 1023
DB 3086 CCATGATCGGAGGCGCTTTCGAGAGCGGTGGCGCATCGACCGCTGACCGCATCGGCAAGA 3145
QY 1024 AGAATTCATCTCTGCGACAGGTGCGAGCATGACCTCAACTCGGGCGTATTTCACAAACC 1083
DB 3146 AGAATTCATCTCTGCGACAGGTGCGAGCATGACCTCAACTCGGGCGTATTTCACAAACC 3205
QY 1084 AGGAAACGCCATCATCCAGGAGATCGTCAAGTACGACCGCGAGATGGTGCAGCAGCGCG 1143
DB 3206 AGGAAACGCCATCATCCAGGAGATCGTCAAGTACGACCGCGAGATGGTGCAGCAGCGCG 3265
QY 1144 AGCTGGGTTCAGCGGTGGGCTCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1203
DB 3266 AGCGGTTCAGCGGTGGGCTCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3325
QY 1204 CCATCGCCACGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1231
DB 3326 TGATCCAGGCAACCTGCGAGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3353

RESULT 12
AAD29757
ID AAD29757 standard; DNA; 4751 BP.
XX AC AAD29757;
XX AC AAD29757;
DT 17-MAY-2002 (first entry)

AC AAH48730;
XX 26-OCT-2001 (first entry)
XX Human HCN4 cDNA.
DE Human; activator; patch-clamp; high through-put screening; inhibitor;
KW hyperpolarization-activated cation channel; HCN4; ss.
XX
XX Homo sapiens.
XX OS
XX Key Location/Qualifiers
XX CDS 587..4178
XX /*tag= a
XX /product= "HCN4"
XX
XX WO200159153-A2.
XX
XX 16-AUG-2001.
XX
XX 24-JAN-2001; 2001WO-EF000755.
XX PF
XX 12-FEB-2000; 2000DE-01006309.
XX PR
XX (AVET) AVENTIS PHARMA DEUT GMBH.
XX PA
XX Jansen H, Brueggemann A, Heitsch H, Goegelein H;
XX WPI; 2001-550023/61.
XX P-PSDB; AAB86462.
XX
XX Identifying substances which modify activity of hyperpolarization-
PT activated cation channels using fluorescent imaging is useful to identify
PT possible therapeutic pharmaceuticals.
XX
XX Disclosure; Page 44-46; 58pp; German.
XX
XX This invention describes a novel method for identifying substances which
CC modify activity of hyperpolarization-activated cation channels (HACC), by
CC placing cells which express an HACC in an iso-osmotic sodium ion-free
CC buffer in the presence of a potential-sensitive fluorescent dye, and
CC measuring membrane potential after the addition of sodium ions. The
CC invention is used to identify activators or inhibitors of HACCs. Unlike
CC prior art patch-clamp techniques, this invention can be automated, and
CC allows high through put screening. This sequence encodes the human
CC hyperpolarization-activated cation channel protein HCN4 which is
XX described in the method of the invention
XX
SQ Sequence 5065 BP; 919 A; 1783 C; 1497 G; 866 T; 0 U; 0 Other;

Query Match 69.1%; Score 927.2; DB 4; Length 5065;
Best Local Similarity 84.7%; Pred. No. 2.9e-156;
Matches 1040; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

QY 4 TGGCGTCCACCAAGATCCTCAGCCTCTGGGGTGTGGCCCTCTCACGCTGATCGGT 63
DB 1696 TCCGCTTCCGAAGATCCTCAGCCTCTTAGCGCTGTACGCTCTCCCGCCTCATTCGAT 1755

QY 64 ACATCATCATGTGGAGGAGATCTCCACATGACCTATGACCTGGCCAGCGGGTGATGA 123
DB 1756 ATATTACCAAGTGGAGAGATCTTCCATGATGACCTAGACCTGGCCAGCGCGGTGTC 1815

QY 124 GGATCTGCAATCTCATCAGCATGATGCTGCTGTCTGCCATGGGACGCGTCCCTGACGT 183
DB 1816 GCATGTGACCTCATCGGCATGATGCTCTGCTCTGCCACTGGGACGCGTGCCTGACGT 1875

QY 184 TCTGTGCCCCTGCTGCAGGACTTCCGGGCAACTGCTGGGTGTCCATCAATGGCATGG 243
DB 1876 TCTGTGTACCATGCTACAGGACTTCCCTGACGACTGCTGGGTGTCCATCAACAAATGG 1935

QY 244 TGAACCACTCGTGGAGTGAATCTGACTCTCTTCCGACTCTTTCAAGGCCATGAGCCATGCG 303
DB 1936 TGAACCACTCTGGGGAGGACGATCTCTCTACGCGCTCTTCAAGGCCATGAGCCATGCG 1995

QY 304 TGTGCATCGGCTACGGCCGGCAGCGCCGAGAGCATGACGAGCATCTGGCTGACCATGC 363
DB 1996 TGTGCATCGGCTACGGCCGGCAGCGCCGAGAGCATGTCGAGCATCTGGCTGACCATGC 2055

QY 364 TCAGCATGATTTGTGGGTGCCACCTGCTACGCAATGTTTCATCGGCCACGCCCTCA 423
DB 2056 TCAGCATGATCGTGGGTGCCACCTGCTACGCAATGTTTCATTTGGCCACGCCCTCA 2115

QY 424 TCCAGTCTGCTGGAATCTCTCGCGGCCAGTACCGAGGAAAGTACAAAGCAGGTGGAGCAGT 483
DB 2116 TCCAGTCTGGAATCTCTCGCGGCCAGTACCGAGGAAAGTACAAAGCAGGTGGAGCAGT 2175

QY 484 ACATGTCTCTTCCACAGCTGCGCAGTGTCTCCGCGAGAGATCCACGACTACTATGAGC 543
DB 2176 ACATGTCTCTTCCACAGCTGCGCAGTGTCTCCGCGAGAGATCCACGACTACTATGAGC 2235

QY 544 ACCGTTACAGGGCAAGATGTTTACGAGGAGCAGCATCTCGGGCAGCTCAACGGGCCCC 603
DB 2236 ACCGTTACAGGGCAAGATGTTTACGAGGAGAGAGCATCTCGGGCAGCTACGAGGCCCC 2295

QY 604 TCGCGGAGGAGATCGTCAACTTCACTGCCGGAAGCTGGTGGCTCTCCATGCCGCTGTTCG 663
DB 2296 TCGCGGAGGAGATCATCAACTTTAACTGTGGAAGCTGGTGGCTCTCCATGCCACTGTTTG 2355

QY 664 CCAAGCCGAGCCCAACTTCTGTCAGGCGCATGCTGACCAAGCTCAAGTTTCGAGGTCTTCC 723
DB 2356 CCAATGCGGAGCCCAACTTCTGTCAGCTGCTGACCAAGCTCGGTTTCGAGGTCTTCC 2415

QY 724 AGCGGGTGACTATCATCATCGCGAAGCACCATCGGGAAGAGATGTACTTTCATCCAGC 783
DB 2416 AGCGGGTGACTATCATCATCGGGAAGCACCATCGGGAAGAGATGTACTTTCATCCAGC 2475

QY 784 AGCGCGTGTGAGCGTGTCTCACTAAGGGAACAAGAGAGATGAAGTGTCCGATGCTCTCT 843
DB 2476 ATGGCGTGTGAGCGTGTCTCACTAAGGGAACAAGAGAGATGAAGTGTCCGATGCTCTCT 2535

QY 844 ACTTCGGGAGATCTGCTCTGCTCACTCCCGGGCCGCGCAGCGAGCGTGGCGCTGACA 903
DB 2536 ACTTCGGGAGATCTGCTCTGCTGCTGACCCCGGGCCGCGCAGCGAGCGTGGCGCTGACA 2595

QY 904 CCTACTCGCGCTCTATTTCGCTGAGCGTGGGACAACTTCAACGAGGTGTGGAGGAGTACC 963
DB 2596 CCTACTCGCGCTCTACTCTGCTGAGCGTGGGACAACTTCAATGAGGTGTGGAGGAGTACC 2655

QY 964 CCATGATCGCGCGCGCTTTCGAGACGCGTGGCCATCGACCGCTTGACCGCATCGGCAAGA 1023
DB 2656 CCATGATCGAAGGCGCTTTCGAGACGCGTGGCGCTGGACCGCTTGACCGCATTTGGCAAGA 2715

QY 1024 AGAATTCATCTCTGCAAGGTGAGCATGACCTCAACTCGGGCGTATTTCACACACC 1083
DB 2716 AGAATTCATCTCTGCAAGGTGAGCATGACCTCAACTCGGGCGTATTTCACACTACC 2775

QY 1084 AGGAAACGCCATCATCCAGGAGATCGTCAAGTACGACCGCGAGATGGTGACGAGCGCG 1143
DB 2776 AGGAAATGAGATCATCCAGCAGATTTGACGATGACCGGAGATGGCCCACTGGCGCG 2835

QY 1144 AGCTGGGCTGACGCGTGGCGCTCTTCCCGCGCGCGCGCGCGCGCGCGCGCATCTCGG 1203
DB 2836 ACCGCGTCCAGGCTGCTGCTCTGCGACCCCAACCCCAACCCCAACCCCGCTCATCTGAGACCCCGC 2895

QY 1204 CCATGCGCACGCTGACGAGCGGGCGGC 1231
DB 2896 TGATCCAGGACCACTGACGGCTGCCGC 2923

RESULT 14
ADR86593
ID ADR86593 standard; cDNA; 5065 BP.
XX
XX ADR86593;
XX
DT 02-DBC-2004 (first entry)


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Db      2968 ACTTTGGAGAGATCTGCTGCTGACCCGGGGCCGGCCACAGCCAGCGTGAGGGCCGACA 3027
Qy      904 CCTACTGCCGCCCTCTATTGGCTGAGCGTGGACAACTTCAACGAGGTGCTGGAGGATACC 963
Db      3028 CCTACTGCCGCCCTCTACTCGCTGAGCGTGGACAACTTCAATGAGGTGCTGGAGGATACC 3087
Qy      964 CCATGATGGCGCGCGCTTTCGAGACGCTGGCCATCGACCGCCTGGACCCGCGCATCGGCAAGA 1023
Db      3088 CCATGATGGCAAGGGCCCTTCGAGACCGTGGCGCTGGACCCGCTGGACCGCATTTGGCAAGA 3147
Qy      1024 AGAATTCATCTCTCTGCAAGGTGAGCATGACCTCAACTCGGGGGTATTCAACAACC 1083
Db      3148 AGAACTCCATCTCTCTCCACAAAGTCCAGCACGACCTCAACTCCGGCGTCTTCAACTACC 3207
Qy      1084 AGGAGAACGCCATCATCCAGGAGATGTCAGGTACGACCGCGGAGATGTCAGCAGGCGCG 1143
Db      3208 AGGAGAAATGAGATCATCCAGCAGATTGTGCAGCATGACCGGGAGATGGCCCACTGCGCGC 3267
Qy      1144 AGCTGGGCTCAGCGCGTGGGCTCTTCCCGCCGCGCGCGCGCGCGCGCGCGAGTCACCTCGG 1203
Db      3268 ACCGGTCCAGGCTGCTGCTCTGCCACCCCAACCCCGCGCGCGCGCGCGCGCGCGCGCGC 3327
Qy      1204 CCATGCCACGCTGCAGCAGCGCGCGCGC 1231
Db      3328 TGATCCAGGCACCACTGCAGGCTGCCGC 3355

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OM nucleic - nucleic search, using sw model
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(without alignments)
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Perfect score: 1342
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: gb_est2.*
- 3: gb_est3.*
- 4: gb_est4.*
- 5: gb_est5.*
- 6: gb_est6.*
- 7: gb_est7.*
- 8: gb_est8.*
- 9: gb_est9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1222.4	91.1	1794	3 BC039619	Homo sapi
2	736.8	54.9	913	6 CA488537	CA488537 AGENCOURT
3	723.2	53.9	829	4 BI490383	BI490383 603031868
4	719	53.6	3226	3 BC039156	BC039156 Mus muscu
5	719	53.6	3265	3 AK032225	AK032225 Mus muscu
6	719	53.6	4015	3 AK082719	AK082719 Mus muscu
7	688.2	51.3	1620	9 AY399924	AY399924 Homo sapi
8	687.4	51.2	815	2 BE546989	BE546989 601071965
9	656.8	48.9	1638	9 AY399926	AY399926 Mus muscu
10	646	48.1	785	4 BG974320	BG974320 602844071
11	587	43.7	707	7 CK358214	CK358214 AGENCOURT
12	585.2	43.6	691	2 AW073171	AW073171 wy94h02.x
13	541	40.3	564	6 CA842988	CA842988 ir27f10.x
14	532.2	39.7	569	6 CB054837	CB054837 NISC_gm06
15	532.2	39.7	569	6 CB054838	CB054838 NISC_gm06
16	531.6	39.6	560	7 CK902966	CK902966 ir27f10.y
17	527	39.3	595	2 BF593827	BF593827 nac05402
18	526.6	39.2	568	1 AL809833	AL809833 wh77g04.x
19	526	39.2	542	7 CK902965	CK902965 ir27f10.x
20	523.6	39.0	659	7 CF253024	CF253024 mdv004.b0
21	483	36.0	520	2 BF510959	BF510959 UI-H-B14-
22	473	35.2	957	6 BV714221	BV714221 BU714221
23	471.4	35.1	1888	3 AK014722	AK014722 Mus muscu
24	462.4	34.5	1120	5 BU956439	BU956439 AGENCOURT

25	455.2	33.9	785	7	CNS28592	UI-M-HQ0-
26	452.6	33.7	1620	9	AY399925	Pan trogl
27	451.8	33.7	780	2	BE260963	601151693
28	446.4	33.3	484	1	AI422949	tf23a05.x
29	443.6	33.1	453	6	CA842473	ir27f10.y
30	438.6	32.7	509	1	AA843273	aj16503.8
31	434.4	32.4	673	6	CB556893	AMGNNUC.N
32	433.8	32.3	954	6	CB201579	AGENCOURT
33	429.8	32.0	702	7	CF531532	UI-M-FY0-
34	425.8	31.7	606	7	CV030457	9582 Full
35	424.4	31.6	499	5	BX279829	BX279829
36	423.2	31.5	1087	2	BE798933	601583714
37	419.6	31.3	1263	9	AY401918	Mus muscu
38	416.8	31.1	858	2	BE793179	601581483
39	411.2	30.6	965	4	BI490063	603031868
40	411	30.6	785	5	BX872016	BX872016
41	403.4	30.1	974	5	BU914463	AGENCOURT
42	391.6	29.2	484	2	BE138253	UG50403.y
43	389.8	29.0	452	5	BX282916	BX282916
44	389.8	29.0	452	7	CR742764	CR742764
45	380.6	28.4	1266	9	AY401916	Homo sapi

ALIGNMENTS

RESULT 1	BC039619	1794 bp	mRNA	linear	HTC 19-NOV-2003
LOCUS	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 2, mRNA (cdna clone IMAGE:5730201).				
DEFINITION	BC039619				
ACCESSION	BC039619.1	GI:24464597			
VERSION	BC039619				
KEYWORDS	HTC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1794)				
AUTHORS	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altshul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.J., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diachenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahy,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butlerfield,Y.S., Krzywinski,M.I., Skalska,U., Smalley,D.E., Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
MEDLINE	22388257				
PUBMED	12477932				
REFERENCE	2 (bases 1 to 1794)				
AUTHORS	Strausberg,R.				
TITLE	Direct Submission				
JOURNAL	Submitted (01-NOV-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov				
COMMENT	Contact: MGC help desk Email: cgabbs-r@mail.nih.gov Tissue Procurement: Invitrogen				

cdNA Library Preparation: Life Technologies, Inc.
cdNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
Contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 84 Row: j Column: 20
This clone has the following problem: no polyA-tail.

FEATURES

Location/Qualifiers
1..1794
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5730201"
/tissue_type="Brain, hippocampus"
/clone_lib="NIH_MGC_124"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 91.1%; Score 1222.4; DB 3; Length 1794;
Best Local Similarity 99.8%; Pred. No. 3.3e-240;
Matches 1245; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 4 TGGGCTTACCAAGATCCCTCAGCCTCTCGGGGTGCTGGGCTCTCAAGCCTGATCCGCT 63
DB 543 TGGGCTTACCAAGATCCCTCAGCCTCTCGGGGTGCTGGGCTCTCAAGCCTGATCCGCT 602

QY 64 ACATCATCAGTGGAGAGATCTTCCACATGACCTATGACCTGGCAGCGGGTGATGA 123
DB 603 ACATCATCAGTGGAGAGATCTTCCACATGACCTATGACCTGGCAGCGGGTGATGA 662

QY 124 GGATCTGCAATCTCATCAGCATGATGCTGCTCTGCGCCTGGGACGGCTGCGTCACT 183
DB 663 GGATCTGCAATCTCATCAGCATGATGCTGCTCTGCGCCTGGGACGGCTGCGTCACT 722

QY 184 TCTGCTGCGCATGCTGCGAGGACTTCCCGGAACTGCTGGGTGTCCATCAATGGCATGG 243
DB 723 TCTGCTGCGCATGCTGCGAGGACTTCCCGGAACTGCTGGGTGTCCATCAATGGCATGG 782

QY 244 TGAACCACTCGTGGAGTGAATGTACTCTTTCGCACTCTTCAAGGCGCATGAGCCATGC 303
DB 783 TGAACCACTCGTGGAGTGAATGTACTCTTTCGCACTCTTCAAGGCGCATGAGCCATGC 842

QY 304 TGTGCTCGGTACGCGCGGAGGCGCGGAGGAGCATGACGACATCTGCTGACCATGC 363
DB 843 TGTGCTCGGTACGCGCGGAGGCGCGGAGGAGCATGACGACATCTGCTGACCATGC 902

QY 364 TCAGCATGATTTGGGTGCGCCTGCTAGCCATGTTTCATCGGCCACGCGCTGCGCCTCA 423
DB 903 TCAGCATGATTTGGGTGCGCCTGCTAGCCATGTTTCATCGGCCACGCGCTGCGCCTCA 962

QY 424 TCAGTCTGCTGGAATCTCTCGCGCGCGAGTACAGGAGAGTACAGAGAGTGGAGCATG 483
DB 963 TCAGTCTGCTGGAATCTCTCGCGCGCGAGTACAGGAGAGTACAGAGAGTGGAGCATG 1022

QY 484 ACATGTCCTTCCACAGCTGCGAGTGAATCTCGCGCAGAGATCCACGACTACTATGAGC 543
DB 1023 ACATGTCCTTCCACAGCTGCGAGTGAATCTCGCGCAGAGATCCACGACTACTATGAGC 1082

QY 544 ACCGTTTACAGGCAAGATGTTTACGAGGAGCATGCTCGGCGAGCTCAACGGGCGCCC 603
DB 1083 ACCGTTTACAGGCAAGATGTTTACGAGGAGCATGCTCGGCGAGCTCAACGGGCGCCC 1142

QY 604 TGGGAGGAGATCGTCAACTTCAATGCGGAGAGTGTGTGCTCCATCGCGCTGTTTCG 663
DB 1143 TGGGAGGAGATCGTCAACTTCAATGCGGAGAGTGTGTGCTCCATCGCGCTGTTTCG 1202

QY 664 CCAACCGCGACCCCACTTCTGTCACGGCCATGCTGACCAAGCTCAAGTTCGAGGTTCTTC 723

DB 1203 CCAACCGCGACCCCAACTTCTGTCACGGCCATGCTGACCAAGCTCAAGTTCGAGGTTCTCC 1262
QY 724 AGCGGGTGAATCATCATATCCGGAAGCACCACCATCGGGAAGAGATGTACTTTCACGAGC 783
DB 1263 AGCGGGTGAATCATCATATCCGGAAGCACCACCATCGGGAAGAGATGTACTTTCACGAGC 1322
QY 784 ACGGGCTGCTCAGGCTGCTCACTAAGGGCAACAAGGAGATGAAGCTGCCATGCTCTCT 843
DB 1323 ACGGGCTGCTCAGGCTGCTCACTAAGGGCAACAAGGAGATGAAGCTGCCATGCTCTCT 1382
QY 844 ACTTCGGGGAGATCTGCTGCTCACTCCCGGGCGCGCCACCGCGAGCTGCGGGGTGACA 903
DB 1383 ACTTCGGGGAGATCTGCTGCTCACTCCCGGGCGCGCCACCGCGAGCTGCGGGCGGACA 1442
QY 904 CCTACTCGCGCTCTATTTCGCTGAGCGTGGAGCAACTTCAACAGAGTGTCTGGAGGATACC 963
DB 1443 CCTACTCGCGCTCTATTTCGCTGAGCGTGGAGCAACTTCAACAGAGTGTCTGGAGGATACC 1502
QY 964 CCATGATCGCGCGCGCTTCGAGAGCGTGGCCATCGACCGCTGAGCCGATCGGCAAGA 1023
DB 1503 CCATGATCGCGCGCGCTTCGAGAGCGTGGCCATCGACCGCTGAGCCGATCGGCAAGA 1562
QY 1024 AGAATTCATCTCTCTGCAAGGTGACAGTACCTCAACTCGGGCGTATTCAACAACC 1083
DB 1563 AGAATTCATCTCTCTGCAAGGTGACAGTACCTCAACTCGGGCGTATTCAACAACC 1622
QY 1084 AGGAAACGCGCATCATCAGGAGATCTCAAGTAGCAGCGGAGATGTGAGCAGGCGG 1143
DB 1623 AGGAAACGCGCATCATCAGGAGATCTCAAGTAGCAGCGGAGATGTGAGCAGGCGG 1682
QY 1144 AGCTGGGCTCAGCGGCTGGGCTCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1202
DB 1683 AGCTGGG-TCAGCGGCTGGGCTCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1741
QY 1203 GCCATCGCACGCTCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 1250
DB 1742 GCCATCGCACGCTCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 1789

RESULT 2
CA488537
LOCUS AGENCOURT_10808788 MAPcL Homo sapiens cdNA clone IMAGE:6720303 5',
DEFINITION mRNA sequence.
ACCESSION CA488537
VERSION CA488537.1 GI:24950678
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 913)
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
cdNA Library Preparation: Invitrogen Corp
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM14279 row: j column: 15
High quality sequence stop: 682.
Location/Qualifiers
1..913
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6720303"

/cell line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
hTERT-HW1, LNCap"
/lab_host="EMDHL08"

/clone_lib="MAPCL"
/note="Vector: pCMV-Sport6; Site 1: EcoRV; Site 2: Not I;
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average
insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Eglund, James J. Vincent, Robert Strausberg,
Bungkook Lee & Ira Pastan: Discovery of new breast
cancer genes encoding membrane and secreted proteins.
Manuscript submitted."

ORIGIN

Query Match 54.9%; Score 736.8; DB 6; Length 913;
Best Local Similarity 96.3%; Pred. No. 1.1e-140;
Matches 787; Conservative 0; Mismatches 23; Indels 7; Gaps 3;

QY 81 GAGATCTTCACATGACCTATGACCTGGCGCGGTGATGAGGATCTGCAATCTCATC 140
DB 1 GAGATCTTCACATGACCTATGACCTGGCGCGGTGATGAGGATCTGCAATCTCATC 60
QY 141 AGCATGATGCTGCTCTGCCACTGGACGGCTGCTGAGTTCCTGTGTCGCAATGCTG 200
DB 61 AGCATGATGCTGCTCTGCCACTGGACGGCTGCTGAGTTCCTGTGTCGCAATGCTG 120
QY 201 CAGGACTTCGCGGCACTGCTGGTGTTCATCAATGGCATGTGTGAACCACTCGTGGAT 260
DB 121 CAGGACTTCGCGGCACTGCTGGTGTTCATCAATGGCATGTGTGAACCACTCGTGGAT 180
QY 261 GAATCTGACTCTTCGCACTCTTCAAGGCCATCAGCCATGCTGTGTCATCGGTCAGCG 320
DB 181 GAATCTGACTCTTCGCACTCTTCAAGGCCATCAGCCATGCTGTGTCATCGGTCAGCG 240
QY 321 CGCAGCGCGCCGAGAGCATGACGGACATCTGGCTGACCAATGCTCAGCATGATTTGGGT 380
DB 241 CGCAGCGCGCCGAGAGCATGACGGACATCTGGCTGACCAATGCTCAGCATGATTTGGGT 300
QY 381 GCCACTGTCTACGCCATGTTTCATCGGCCAGCCACTGCTCTCATCGCTGCTGGACTCC 440
DB 301 GCCACTGTCTACGCCATGTTTCATCGGCCAGCCACTGCTCTCATCGCTGCTGGACTCC 360
QY 441 TCGCGGCGCCAGTACAGGAGAGTACAAGCAGTGGAGCATGCTCTTCCCAAG 500
DB 361 TCGCGGCGCCAGTACAGGAGAGTACAAGCAGTGGAGCATGCTCTTCCCAAG 420
QY 501 CTGCGAGCTGACTTCCGCGAGAGATCCACGACTACTATGAGCACCGTTACCGAGGCAAG 560
DB 421 CTGCGAGCTGACTTCCGCGAGAGATCCACGACTACTATGAGCACCGTTACCGAGGCAAG 480
QY 561 ATGTTTTCAGGAGCAGCATCTTGGCGAGCTCAACGGGCCCTTGGCGGAGGAGATGCTC 620
DB 481 ATGTTTTCAGGAGCAGCATCTTGGCGAGCTCAACGGGCCCTTGGCGGAGGAGATGCTC 540
QY 621 AACTTCAACTGCGGAGAGCTGGTGGCTTCATGCGCTGTTCGCAACGCTGACCCCAAC 680
DB 541 AACTTCAACTGCGGAGAGCTGGTGGCTTCATGCGCTGTTCGCAACGCTGACCCCAAC 600
QY 681 TTGCTCACGGCGCATGCTGACCAAGCTCAAGTTCGAGGTCTTCCAGCGGGTGAATCATC 740
DB 601 TTGCTCACGGCGCATGCTGACCAAGCTCAAGTTCGAGGTCTTCCAGCGGGTGAATCATC 660
QY 741 ATCCGGAAGGCA - CCAATCGGGAAGAAGATGTAATTCATCAGCA CGGCGTGTGTCAGCGT 799
DB 661 ATCCGGAAGGCA CCAATCGGGAAGAAGATGTAATTCATCAGCA CGGCGTGTGTCAGCGT 720
QY 800 GCTCACTAAGGCGCAACAG - GAGATGAGCTGTCCGATGCTCTACTTTCGGGGAGATCT 858
DB 721 GCTCACTAAGGCGCAACAGATGATAAACTGTCCGATGGCTCTTAATCTTCGGGGAGAT 780
QY 859 GCCTGCT-----CACCCGGGGCCCGCCGACGGCGAGC 890
DB 781 CTGCGCTGCTCCACCCGGGGCCCGCCGACGGCGAGC 817

RESULT 3

BI490383/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BI490383 829 bp mRNA linear EST 28-AUG-2001
603031868R1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5172928 3',
mRNA sequence.
BI490383
BI490383.1 GI:15329611
EST.
Homo sapiens (human)

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Inyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>
Plate: LLAM11430 row: h column: 17

High quality sequence stop: 824.
Location/Qualifiers

1. .829

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5172928"

/lab_host="DH10B"

/clone_lib="NIH MGC 115"

/note="Organ: pooled brain, lung, testis; Vector:

pCMV-Sport6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA

source anonymous pool of 6 male brains, age range 23-27; 1

male lung, age 27; and 1 male testis, age 69. Library is

oligo-dr primed and directionally cloned (EcoRV site is

destroyed upon cloning). Average insert size 1.8 kb,

insert size range 1-3 kb. Library is normalized and

enriched for full-length clones and was constructed by C.

Gruber (Invitrogen). Research Genetics tracking code

021. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 53.9%; Score 723.2; DB 4; Length 829;
Best Local Similarity 98.7%; Pred. No. 7e-138;
Matches 813; Conservative 0; Mismatches 3; Indels 8; Gaps 8;

QY 432 CTGACTCTCTCGCGGCCAG - TACCAGGAGAGTACAGCAGGTGAGCAGTACATGTC 490

DB 825 CTGACTCTCTCGCGGCCAGTTACCAGGAGAGTACAAGCA - GTGGACAGTACATGTC 767

QY 491 CTTCCACAGCTGCCAGC - TGACTTCCGCCAGAGAT - CCACGACTACTATGACACCGT 548

DB 766 CTGCCACAAGCTGCCAGCTGACTTCCGCCAGAGATCCACGACTACTATGAGCAGCG - 708

QY 549 TACCAGGCAAGATGTTTTCAGCAGGAGCAGCA - TCCTGGGCGAGCTCAACGGGCCCCCTGGC 607

DB 707 TACCAGGCCAGATGTTTTCAGCAGGAGCAGCATTCCTGGGCGAGCTCAACGGGCCCCCTGGC 648

QY 608 GAGGAGAGTCTGCAACTTCAACTGCGGAGCTGTGTGGCTCCATCGCGCTGTTCGCAA 667

DB 647 GAGGAGAGTCTGCAACTTCAACTGCGGAGCTGTGTGGCTCCATCGCGCTGTTCGCAA 588

QY 668 CGCGGACCCCACTTCTGTCACGGCCATGTGACCAAGCTCAAGTTCAGAGTCTTCAGGCC 727

DB 587 CGCGGACCCCACTTCTGTCACGGCCATGTGACCAAGCTCAAGTTCAGAGTCTTCAGGCC 528

QY 728 GGTGACTACATCATCCGGAAGGACCATCGGAAGAAGATGTACTTTCATCCAGCAG 787
 Db |||||||
 QY 527 GGTGACTACATCATCCGGAAGGACCATCGGAAGAAGATGTACTTTCATCCAGCAG 468
 Db |||||||
 QY 788 CGTGGTACGCGTCTCACTAAGGGCAACAAAGGAGATGAAGCTGTCCGATGGCTCTACTT 847
 Db |||||||
 QY 467 CGTGGTACGCGTCTCACTAAGGGCAACAAAGGAGATGAAGCTGTCCGATGGCTCTACTT 408
 Db |||||||
 QY 848 CGGGAGATCTGCTCTCACTAAGGGCAACAAAGGAGATGAAGCTGTCCGATGGCTCTACTT 907
 Db |||||||
 QY 407 CGGGAGATCTGCTCTCACTAAGGGCAACAAAGGAGATGAAGCTGTCCGATGGCTCTACTT 348
 Db |||||||
 QY 908 CTGCGCCCTCTATTCGCTGAGCGTGGACAACTTCAACGAGGTGCTGGAGGATACCCAT 967
 Db |||||||
 QY 347 CTGCGCCCTCTATTCGCTGAGCGTGGACAACTTCAACGAGGTGCTGGAGGATACCCAT 288
 Db |||||||
 QY 968 GATGCGCGCGCTTCGAGACGCTGGCCATCGACCGCTGGACCGCATCGCAAGAAGAA 1027
 Db |||||||
 QY 287 GATGCGCGCGCTTCGAGACGCTGGCCATCGACCGCTGGACCGCATCGCAAGAAGAA 228
 Db |||||||
 QY 1028 TTCCATCTCTGACACAGGTGAGCATGACCTCAACTCGGGGTATTTCAACACAGGA 1087
 Db |||||||
 QY 227 TTCCATCTCTGACACAGGTGAGCATGACCTCAACTCGGGGTATTTCAACACAGGA 168
 Db |||||||
 QY 1088 GAACGCATCATCCAGGAGATCGTCAAGTACGACCGCGAGATGTCAGCAGCGCAGCT 1147
 Db |||||||
 QY 167 GAACGCATCATCCAGGAGATCGTCAAGTACGACCGCGAGATGTCAGCAGCGCAGCT 108
 Db |||||||
 QY 1148 GGGCTCAGCGCGTGGGCTCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1206
 Db |||||||
 QY 107 GGG-TCAGCGCGTGGGCTCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 49
 Db |||||||
 QY 1207 TGCCACGCTGACGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1250
 Db |||||||
 QY 48 TGCCACGCTGACGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5

RESULT 4
 BC039156
 LOCUS
 DEFINITION
 Mus musculus, 3226 bp mRNA linear HTC 06-NOV-2002
 nucleotide-gated K+ 3, clone IMAGE:4511289, mRNA.
 ACCESSION
 BC039156
 VERSION
 BC039156.1 GI:24657642
 KEYWORDS
 HTC.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 3226)
 Strausberg, R.
 Direct Submission
 Submitted (01-NOV-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: ang@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louseged, H.,
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
 A.N., Gibbs, R.A.
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 31 Row: n Column: 14
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 6680190
 This clone has the following problem: frame shifted.

FEATURES
 Location/Qualifiers
 1..3226
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:4511289"
 /tissue type="Eye, retina, mouse strain C57BL/6"
 /clone_lib="NIH MGC_94"
 /lab_host="DH10B"
 /note="Vector: PCMV-SPORT6"

ORIGIN
 Query Match 53.6%; Score 719; DB 3; Length 3226;
 Best Local Similarity 80.8%; Pred. No. 5.8e-137;
 Matches 839; Conservative 0; Mismatches 200; Indels 0; Gaps 0;
 QY 7 GCTTACCAAGATCTCAGCCTCTCGCGCTGCTGCGCTCTCAGCCCTGATCCGCTACA 66
 Db 671 GATTACCAAGATCTTACGCTGCTGCGCTGCTCCTCCGCTCATCCGCTACA 730
 QY 67 TCCATCAGTGGAGGAGATCTTCCACATGACCTAGCTGCGCAGCGCGGTGATGAGA 126
 Db 731 TACACCATGGAGGAGATCTTACATGACCTAGCAGCTGCGCAGTGCAGTGGTTCGA 790
 QY 127 TCTCAATCTCATCAGCATGATGCTGCTGCTCTGCACTGGGAGCGCTGCTGCACTTCC 186
 Db 791 TCTTCAACCTCATTGGATGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 850
 QY 187 TGTGCCCCATGCTGAGGACTTCCCGCGCAACTGCTGCTGCTGCTGCTGCTGCTGCTG 246
 Db 851 TGTGCTCTATGCTGAGGACTTCCCGTCCGACTGCTGCTGCTGCTGCTGCTGCTGCTG 910
 QY 247 ACCACTGCTGAGTGAAGTACTTCTTCCGCACTCTTCAAGGCCATGAGCAGCATGCTGT 306
 Db 911 ACCACTGCTGAGGCGCGCAGTATTTCCACGCGCTGTTCAAGGCCATGAGTACATGCTAT 970
 QY 307 GCATCGGATGCG 366
 Db 971 GCATTTGCTATGGGCG 1030
 QY 367 GCATGATTTGGGTGCGCACCTGCTGACGCAATGTTTCATCGGCGCAGCGCACTGCTCATCC 426
 Db 1031 GTATGATTTGGGTGCGCACCTGCTGACGCAATGTTTCATCGGCGCAGCGCGCGCGCGCG 1090
 QY 427 AGTGGCTGACTCTTCCG 486
 Db 1091 AGTCCCTGGATCTTTCG 1150
 QY 487 TGTCTCTTCCCAAGCTGCGCAGCTGACTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 546
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 Mus musculus adult male olfactory brain cDNA, RIKEN full-length
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 product:hyperpolarization-activated, cyclic nucleotide-gated K+ 3,
 full insert sequence.

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 HTC; CAP trapper.
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 99279253
 10349636

2
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 20499374
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3
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 Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohata, E., Watahiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multipillar sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
 11076861

4
 The RIKEN Genome Exploration Research Group Phase II Team and the
 FANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)

5
 The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
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 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 3265)

AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
 Hayashida, K., Hayate, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
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 Muramatsu, M. and Hayashizaki, Y.

TITLE
 JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.jp/
 URL: http://phantom.gsc.riken.jp/.

FEATURES
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prepare mouse tissues.
Please visit our web site for further details.
URL:<http://genome.gsc.riken.jp/>
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VERSION	AY139924.1		
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ORGANISM	Homo sapiens		
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AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B., Farrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Carroll,M.		

TITLE	TOTAL
Adams, H.B., and Cargill, J.F. 1960-1963 (2003) Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios	Science 302 (5652)
TOTAL	1960-1963 (2003)

JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBLISHED
14671302
2 (bases 1 to 1620)
REFERENCE
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cardelli, M.

TITLE	COMMENT
<p>Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment.</p>	

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AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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 Endocrine Pancreas Consortium
 Unpublished (2000)
 Other ESTs: ir27f10.y1
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
 Washington University Genome Sequencing Center For information on
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 (hinoue@im.wustl.edu)
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 Amplified once. Contact information: Hiroshi Inoue, MD,
 Metabolism Div. (Alan Permutt Lab), Washington University
 School of Medicine, Box 8127, 660 South Euclid Ave., St.
 Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
 314-362-1916, Fax: 314-747-2692."

FEATURES

source

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 VERSION
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 569)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabp@mail.nih.gov
 cDNA Library Preparation:
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC)
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 info@image.llnl.gov
 Plate: LLAM8061 row: I column: 10

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TGTACCAATCTGAAGTGGAGCGCGCATATCTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

ORIGIN
Query Match 39.7%; Score 532.2; DB 6; Length 569;
Best Local Similarity 99.1%; Pred. No. 9.8e-99;
Matches 556; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

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IMAGE:3291729 5', mRNA sequence.
ACCESSION CB054838
VERSION CB054838.1 GI:27793125

KEYWORDS
SOURCE ORGANISM
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 569)
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs@mail.nih.gov
  CDNA Library Preparation:
  CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LNML
  DNA Sequencing by: National Institutes of Health Intramural
  Sequencing Center (NISC)
  Clone distribution: NCI-CGAP clone distribution information can be
  found through the I.M.A.G.E. Consortium/LNML at:
  info@image.llnl.gov
  Plate: LLAM8061 row: I column: 10
  Seq primer: M13RPI reverse primer (ABI).

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  /note="Organ: Brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCTGAAGTGGAGCGCGCATATCTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

ORIGIN
Query Match 39.7%; Score 532.2; DB 6; Length 569;
Best Local Similarity 99.1%; Pred. No. 9.8e-99;
Matches 556; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 691 CCATGCTGACCAAGCTCAAGTTCGAGTCTTCCAGCGGGTGACTACATCATCCGCGAAG 750
DB 5 CGAGGCTGACCAAGCTCAAGTTCGAGTCTTCCAGCGGGTGACTACATCATCCGCGAAG 64

QY 751 GCACCATCGGGAAGAGATGTACTTTCATCAGACGCGCGTGTGAGGCTCTCACTAAGG 810
DB 65 GCACCATCGGGAAGAGATGTACTTTCATCAGACGCGCGTGTGAGGCTCTCACTAAGG 124

QY 811 GCAACAAGGAGATGAAGCTGTCCGATGGCTCTTACTTTCGCGGAGATCTGCTCTCACCC 870
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QY 871 GGGGCCCGCGACGCGGAGGTGGCGGTGACACCTACTCCGCTTATTCGCTGAGCG 930
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DB 305 TGGCCATCGACCGCTTGACCGCATCGGCAAGAGAAATTCATCTCTTGCACAAGGTGC 364

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Db |||||
Qy 1171 CGCGCGCGCGCGCGCGCGCA-GTCACCTGGGCCATGCCACACGCTGCAGCAGGCGG 1229
Db 484 CGCGCGCGCGCGCGCGCGAGTCACTCGGCCATGCCACACGCTGCAGCAGGCGG 543
Qy 1230 GCCATGAGCTTCTGCCCGCAG 1250
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Qy 544 GCCATGAGCTTCTGCCCGCAG 564
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Job time : 4778 secs

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Run on: October 5, 2005, 22:11:29 ; Search time 254 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues
Total number of hits satisfying chosen parameters: 2405568

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1297	96.6	3372	4	US-09-949-016-165
3	1207	89.9	1792	4	US-09-086-436-40
4	1194.4	89.0	1790	4	US-08-997-685A-11
5	927.2	69.1	4276	4	US-09-949-016-4900
6	927.2	69.1	5065	4	US-09-949-016-744
7	874.2	65.1	1512	4	US-09-086-436-32
8	871	64.9	1584	4	US-08-997-685A-3
9	751.8	56.0	2976	4	US-09-774-528-317
10	735.2	54.8	2733	4	US-08-997-685A-1
11	706	52.6	1518	4	US-09-086-436-34
12	688.8	51.3	1507	4	US-08-997-685A-5
13	680.2	50.7	2246	4	US-09-086-436-38
14	680.2	50.7	2263	4	US-08-997-685A-9
15	680.2	50.7	3224	4	US-09-774-528-238
16	666.6	49.7	1307	3	US-09-172-422-3
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22	221.6	16.5	601	4	US-09-949-016-47503
23	221.2	16.5	601	4	US-09-949-016-21136
24	221.2	16.5	601	4	US-09-949-016-47504
25	211	15.7	601	4	US-09-949-016-21154
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ALIGNMENTS

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; Sequence 1392, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT FILING DATE: 2000-04-14
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1392
; LENGTH: 3235
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-1392

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Best Local Similarity	99.1%	Pred. No. 1.9e-257;		
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Gaps	3;			
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QY	304	TGTGTCATCGGGTACGGCCGCGCAGCGCCGAGAGCATGACGGACATCTGGCTGACCATGC	363	

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; Sequence 40, Application US/09086436
; Patent No. 6703485
; GENERAL INFORMATION:
; APPLICANT: Kandel, Eric R.
; APPLICANT: Santoro, Bina
; APPLICANT: Bartesch, Dusan
; APPLICANT: Siegelbaum, Steven
; APPLICANT: Tibbs, Gareth
; APPLICANT: Grant, Seth
; TITLE OF INVENTION: Brain or Heart Cyclic Nucleotide Gated Ion Channel and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 0575/54806-A
; CURRENT APPLICATION NUMBER: US/09/086,436
; CURRENT FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 67
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; SEQ ID NO 40
; LENGTH: 1792
; TYPE: DNA
; ORGANISM: Human
US-09-086-436-40

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Best Local Similarity 99.0%; Pred. No. 1.le-238;
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QY 124 GGATCTGCAATCTCATCAGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 183
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RESULT 4

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; Sequence 11, Application US/08997685A
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; APPLICANT: The Trustees of Columbia University
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
; FILE REFERENCE: 0575/54806
; CURRENT APPLICATION NUMBER: US/08/997,685A
; CURRENT FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1790
; TYPE: DNA
; ORGANISM: human;
US-08-997-685A-11

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Best Local Similarity 98.9%; Pred. No. 4.2e-236;
Matches 1234; Conservative 0; Mismatches 11; Indels 3; Gaps 3;

QY 4 TCGGCTTCAACCAAGATCTCTAGCTCTCTCGCGCTGTCGGCTCTCAAGCTGATCCGCT 63
Db 540 TCGGCTTCAACCAAAATCTCTAGCTCTCTCGCGCTGTCGGCTCTCAAGCTGATCCGCT 599
QY 64 ACATCCATCAGTGGGAGGATCTTCCACATGACCTATGACCTGCGCGAGCGGCGGTGATGA 123
Db 600 ACATCCATCAGTGGGAGGATCTTCCACATGACCTATGACCTGCGCGAGCGGCGGTGATGA 659
QY 124 GGATCTGCAATCTCATCAGCATGATGCTGCTCTGCGCACTGCGAGCGGCTGCTGCACT 183
Db 660 GGATCTGCAATCTCATCAGCATGATGCTGCTCTGCGCACTGCGAGCGGCTGCTGCACT 719
QY 184 TCTGTGTGCCATGCTGCAAGGACTTCCCGCGCAACTGCTGGGTGCTCCATATGGGATGG 243
Db 720 TCTGTGTGCTATGCTGCAAGGACTTCCCGCGCAACTGCTGGGTGCTCCATATGGGATGG 779
QY 244 TGACCACTCGTGGAGTGAATCTCTGCACTCTTCAAGGCGCATGAGCCCATGC 303
Db 780 TGACCACTCGTGGAGTGAATCTCTGCACTCTTCAAGGCGCATGAGCCCATGC 839
QY 304 TGTGATCGGGTACGGCGCGGAGGAGGATGACGACATCTGGCTGACCATGC 363
Db 840 TGTGATCGGGTACGGCGCGGAGGAGGATGACGACATCTGGCTGACCATGC 899
QY 364 TCAGCATGATGTTGGGTGCCACTGCTGATCGCATGTTATCGGCGCAAGCGCATGCGCTCA 423
Db 900 TCAGCATGATGTTGGGTGCCACTGCTGATCGCATGTTATCGGCGCAAGCGCATGCGCTCA 959
QY 424 TCCAGTCTGCTGACTCTCGCGCGCGGAGTACAGGAGGATGACGAGGAGTGGAGCAGT 483
Db 960 TCCAGTCTGCTGACTCTCGCGCGCGGAGTACAGGAGGATGACGAGGAGTGGAGCAGT 1019
QY 484 ACATGTCCTTCCACAAAGCTGCCAGTGAATTCGCGCGAGAGATCCACGACTACTATGAGC 543
Db 1020 ACATGTCCTTCCACAAAGCTGCCAGTGAATTCGCGCGAGAGATCCACGACTACTATGAGC 1079

QY 544 ACCGTTACCGGCGAAGATGTTTGAAGAGAGAGATCCTGGGAGAGCTCAACGGGCCCC 603
Db 1080 ACCGTTACCGGCGAAGATGTTTGAAGAGAGAGATCCTGGGAGAGCTCAACGGGCCCC 1139
QY 604 TCGGGAGAGATCGTCAACTTCAACTCCCGAAGCTGTTGGCTTCCATGCGGCTGTTTCG 663
Db 1140 TCGGGAGAGATCGTCAACTTCAACTCCCGAAGCTGTTGGCTTCCATGCGGCTGTTTCG 1199
QY 664 CCAACGCGACCCCAACTTTCGTCAGCGCATGCTGACCAAGTCAAGTTCAGAGTCTTCC 723
Db 1200 CCAACGCGACCCCAACTTTCGTCAGCGCATGCTGACCAAGTCAAGTTCAGAGTCTTCC 1259
QY 724 AGCGGGTGAATACATCATCCGGAAGGACATCCGGAAGAGATGATGATTCATCCAGC 783
Db 1260 AGCGGGTGAATACATCATCCGGAAGGACATCCGGAAGAGATGATGATTCATCCAGC 1319
QY 784 ACGGCTGCTCAGCGTGTCTCACTAAGGCAACAAGAGATGAAGTGTCCGATGCTCTCT 843
Db 1320 ACGGCTGCTCAGCGTGTCTCACTAAGGCAACAAGAGATGAAGTGTCCGATGCTCTCT 1379
QY 844 ACTTCGGGAGATCTGCTGTCTCACTCCCGGGCGCGCGCACGCGAGCGTGGGGCTGACA 903
Db 1380 ACTTCGGGAGATCTGCTGTCTCACTCCCGGGCGCGCGCACGCGCA-CGTGGGGCTGACA 1438
QY 904 CTTACTGCGGCTCTATTTCGCTGAGCTGAGCTGAGCAACTTCAACGAGTGTCTGGAGGATCC 963
Db 1439 CTTACTGCGGCTCTATTTCGCTGAGCTGAGCAACTTCAACGAGTGTCTGGAGGATCC 1498
QY 964 CCATGATCGCGCGGCTTCGAGACGCTGGGCACTGACGCGCTGACCGCATCCGCAAGA 1023
Db 1499 CCATGATCGCGGCGCTTCGAGACGCTGGGCACTGACGCGCTGACCGCATCCGCAAGA 1558
QY 1024 AGAATTCATCTCTCTGCAAGGTGTCAGCATGACCTCAACTCGGGCGTATTTCAACAACC 1083
Db 1559 AGAATTCATCTCTCTGCAAGGTGTCAGCATGACCTCAACTCGGGCGTATTTCAACAACC 1618
QY 1084 AGGAGAACCCATCATCCAGGAGATCTCAAGTACGACCGGAGATGTCGAGCAGGCGG 1143
Db 1619 AGGAGAACCCATCATCCAGGAGATCTCAAGTACGACCGGAGATGTCGAGCAGGCGG 1678
QY 1144 AGCTGGGCTCAGCGGCTGGGCTCTTCCCGCGCGCGCGCGCGCGCA-GTCACTCG 1202
Db 1679 AGCTGGG-TCAGCGGCTGGGCTTTTCCCGCGCGCGCGCGCGCGCGCGCGAGTCACTTCG 1737
QY 1203 GCCATCGCACGCTGTCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGAGTTCGCGCGCAG 1250
Db 1738 GCCATCGCACGCTGTCAGCAGCGCGCGCGCGCGCGCGCGCGCGAGTTCGCGCGCAG 1785

RESULT 5

US-09-949-016-4900
; Sequence 4900, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4900
; LENGTH: 4276
; TYPE: DNA
; ORGANISM: Human

US-09-949-016-4900

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Query Match      69.1%; Score 927.2; DB 4; Length 4276;
Best Local Similarity 84.7%; Pred. No. 3.6e-181;
Matches 1040; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

QY      4  TGGCTTTCACCAAGATCCTCAGCCTCTCTGGGCTGCTGGCCCTCTCAGCCCTGATCCGCT 63
DB      849  TCGCTTTCAGGAATCCTCAGCCTCTTAGCCTGTTAGCCTCTCCGCTCTCCGCTCATTCGAT 908

QY      64  ACATCCATCAGTGGGAGAGATCTTCCATGACCTATGACCTTGGCCAGCGCGGTGATGA 123
DB      909  ATATTACCAAGTGGGAAGAGATCTTCCATGACCTACGACCTGGCCAGCGCGGTGATG 968

QY      124  GATCTGCAATCTCATCAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 183
DB      969  GCATCGTGAACCTCATCGGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1028

QY      184  TCGTGGTGGCCATGCTGACGACTTCCCGGCAACTGCTGGGTGTCCATCAATGGGATGG 243
DB      1029  TCGTGGTGGCCATGCTGACGACTTCCCTGACGACTGCTGGGTGTCCATCAACATGG 1088

QY      244  TGAACCACTCGTGGAGTGAATGCTGCTTCCGCTTCCGCTTTCAGGGCCATGAGCCATGC 303
DB      1089  TGAACCACTCTGGGGAAGCAGTACTCTTACGCTCTTCAAGGCCATGAGCCATGC 1148

QY      304  TGTGCTCGGGTACGGCCGCGAGCGCCGAGAGCATGACGGACATCTGCTGACCATGC 363
DB      1149  TGTGCTCGGGTACGGCCGCGAGCGCCGCTGGGCATGTCGCGCTGCTGCTGCTGCTGCTGCT 1208

QY      364  TCAGCATGTTGGGTGGCCACTGCTTACGCCATGTTTCATCGGCGCCGCTGCTGCTGCTGCT 423
DB      1209  TCAGCATGTTGGGTGGCCACTGCTTACGCCATGTTTCATCGGCGCCGCTGCTGCTGCTGCT 1268

QY      424  TCAGTCTGCTGCTGCTTCCGCGGCGCAGTACAGGAGAGTACAGGAGAGTGGAGCAGT 483
DB      1269  TCAGTCTGCTGCTGCTTCCGCGGCGCAGTACAGGAGAGTACAGGAGAGTGGAGCAGT 1328

QY      484  ACATGCTCTTCCAAAGCTGCGAGTGCATCTTCGCGCAGAGATCCAGGACTACTATGAGC 543
DB      1329  ACATGCTCTTCCAAAGCTGCGAGTGCATCTTCGCGCAGAGATCCAGGACTACTATGAGC 1388

QY      544  ACCGTTACCAAGGCAAGATGTTTACAGGAGAGATCCTCGGCGAGCTCAACGGGCCCC 603
DB      1389  ACCGTTACCAAGGCAAGATGTTTACAGGAGAGATCCTCGGCGAGCTCAACGGGCCCC 1448

QY      604  TCGCGGAGGAGATCGTCAACTTCAACTGCGGAGAGCTGCTGGCTCCATGCGCTGTTG 663
DB      1449  TCGCGGAGGAGATCATCACTTTAACTGTCGAGAGCTGCTGGCTCCATGCGCTGTTG 1508

QY      664  CCAACGCGGAGCCCAACTTGTGTCAGGCTGCTGTCAGCAAGCTCAAGTTGAGGTCTTCC 723
DB      1509  CCAATCGGAGCCCAACTTGTGTCAGGCTGCTGTCAGCAAGCTGCTGAGGTCTTCC 1568

QY      724  AGCGGCTGACTATCATCTCGGAGGAGCCATCGGAGAGAGATGCTTCTATCCAGC 783
DB      1569  AGCGTGGGAGTATCATCTCGGAGGAGCCATCGGAGAGAGATGCTTCTATCCAGC 1628

QY      784  ACGGCTGCTGCTGCTGCTCACTAAGGCAACAGGAGAGTGAAGCTGTCCGATGGCTCCT 843
DB      1629  ATGGCTGCTGCTGCTGCTCACTAAGGCAACAGGAGAGTGAAGCTGTCCGATGGCTCCT 1688

QY      844  ACTTGGGAGATCTGCTGCTCAACCGGGGCGCGCAGCGGAGGCTGCGGGCTGACA 903
DB      1689  ACTTGGAGAGATCTGCTGCTGCTCAACCGGGGCGCGCAGCGGAGGCTGCGGGCTGACA 1748

QY      904  CTTACTGCGGCTCTATTGCTGAGCTGAGCTGGAACCTTCAACGAGGTGCTGGAGGATACC 963
DB      1749  CTTACTGCGGCTCTATTGCTGAGCTGAGCTGGAACCTTCAACGAGGTGCTGGAGGATACC 1808

QY      964  CCATGATCGGCGGCTTTCAGAGCGGTGGCCATCGACCGGCTGAGCCGCTGAGCCGCAAGA 1023
DB      1809  CCATGATCGGAGGCTTTCAGAGCGGTGGCCATCGACCGGCTGAGCCGCTGAGCCGCAAGA 1868
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QY      1024  AGAATTTCATCTCTCTGCACAAAGTGCAGCATGACTCACTCGGGCGTATTCAACAACC 1083
DB      1869  AGAATTTCATCTCTCTGCACAAAGTGCAGCATGACTCACTCGGGCGTATTCAACAACC 1928

QY      1084  AGGAGAACGCCATCATCTCAGGAGATGCTCAAGTACGACCGCGAGATGGTGCAGCAGCGG 1143
DB      1929  AGGAGAAATGAGATCATCTCAGCAGATGTTGTCAGCATGACCGGAGATGGCCCACTGCGCG 1988

QY      1144  ACCTGGGCTCAGCGGTGGGCTCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1203
DB      1989  ACCGCTTCAGGCTGCTGCTCTGCCACCCCAACCCCAACCCCAACCCCAACCCCAACCC 2048

QY      1204  CCATCGCCACGCTGCAGCAGCGCGCGCG 1231
DB      2049  TGATCCAGGCACCACTGCAGGCTGCGCG 2076

RESULT 6
US-09-949-016-744
; Sequence 744, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 744
; LENGTH: 5065
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-744

Query Match      69.1%; Score 927.2; DB 4; Length 5065;
Best Local Similarity 84.7%; Pred. No. 3.8e-181;
Matches 1040; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

QY      4  TCGCTTTCACCAAGATCCTCAGCCTCTCTGGGCTGCTGGCCCTCTCAGCCCTGATCCGCT 63
DB      1696  TCGCTTTCACCAAGATCCTCAGCCTCTCTGGGCTGCTGGCCCTCTCAGCCCTCATTCGAT 1755

QY      64  ACATCCATCAGTGGGAGAGATCTTCCATGACCTATGACCTGGCGCGCGGTGATGA 123
DB      1756  ATATTACCAAGTGGGAGAGATCTTCCATGACCTATGACCTGGCGCGCGGTGATGA 1815

QY      124  GGATCTGCAATCTCATCAGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 183
DB      1816  GCATCTGGAACCTCATCGGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1875

QY      184  TCTTGGTGGCCATGCTGCGAGGACTTCCCGGCGCAACTGCTGGGTGTCCATCAATGGGATGG 243
DB      1876  TCTTGGTGGCCATGCTGCGAGGACTTCCCTGACGACTGCTGGGTGTCCATCAACCAACATGG 1935

QY      244  TGAACCACTCGTGGAGTGAATGCTTCTTCCCTTCCACTTTCAGGGCCATGAGCCACATGC 303
DB      1936  TGAACCACTCTCGGGGGAAGCAGTACTCTTACGCGCTCTTCAAGGCCATGAGCCACATGC 1995

QY      304  TGTGATCGGGTACGGCCGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 363
DB      1996  TGTGATCGGGTACGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2055

QY      364  TCAGCATGATGTTGGGTGCGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 423
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Db 2056 TCAGCATGATCGTGGGTGCCACCTGCTAGCCATGTTTATTGGCCAGCCACTGCGCTCA 2115
 QY 424 TCAGTTCGTGACTCTCGCGCGCCAGTA CCAGGAGAGTACAAAGCAGGTGGAGCAT 483
 Db 2116 TCAGTTCGTGACTCTCGCGCGCCAGTAC CAGGAAAGTACAAAGCAGGTGGAGCAT 2175
 QY 484 ACATGTCCTTCCACAGCTGCCAGTGTACTTCGGCCAGAGATCCAGACTACTATGAGC 543
 Db 2176 ACATGTCCTTCCACAGCTGCCAGTGTACTTCGGCCAGAGATCCAGACTACTATGAGC 2235
 QY 544 ACCGTTACAGGCGCAAGATGTTTACGAGGACAGCATCTCGCGCGAGCTCAACGGGCGCC 603
 Db 2236 ACCGTTACAGGCGCAAGATGTTTACGAGGAGAGCATCTCGCGCGAGCTTAAGCGGCGCC 2295
 QY 604 TCGGGAGAGATCGTCAACTTCAACTGCGGAGAGCTGTGCGCTCCATGCCGCTGTTG 663
 Db 2296 TCGGGAGAGATCATCAACTTTAACTGTGCGAAGCTGTGCGCTCCATGCCACTGTTT 2355
 QY 664 CCNACGCCAGCCCAACTTGTGTCAGGCCATGCTGACCAAGCTCAAGTTTCGAGGCTTCC 723
 Db 2356 CCNATCGGAGCCCAACTTGTGTCAGGCCATGCTGACCAAGCTGCGTTTTCGAGGCTTCC 2415
 QY 724 AGCGGGTGACTACATCATCTCCGGAAGGACCATCGGGAAGAGATGTAATTCATCCAGC 783
 Db 2416 AGCGGGTGACTACATCATCTCCGGAAGGACCATCTGGCAAGAGATGTAATTCATCCAGC 2475
 QY 784 AGCGGTGTGTCAGCGTGCTCACTAAGGGCAACAAAGAGAGATGAAGTGTCCGATGGCTCT 843
 Db 2476 ATGGCGTGTGTCAGCGTGCTCACTAAGGGCAACAAAGAGAGATGAAGTGTCCGATGGCTCT 2535
 QY 844 ACTTCGGGAGATCTGCTGCTCACCAGGCGCGCGGCGGAGCGTGGCGGCTGACA 903
 Db 2536 ACTTCGGGAGATCTGCTGCTCACCAGGCGCGCGGCGGAGCGTGGCGGCGGACA 2595
 QY 904 CTTACTGCGCGCTTATTGCTGAGGTGAGCAAACTTCAACGAGGTGCTGGAGGAGTACC 963
 Db 2596 CTTACTGCGCGCTTATTGCTGAGGTGAGCAAACTTCAACGAGGTGCTGGAGGAGTACC 2655
 QY 964 CCATGATGCGGCGCGCTTTCGAGAGCGGTGGCCATCGACCGCTGGACCGCATCGGCAAGA 1023
 Db 2656 CCATGATGCGGAGGCGCTTTCGAGAGCGGTGGCCATCGACCGCTGGACCGCATCGGCAAGA 2715
 QY 1024 AGAATTCATCTCTTCGACAGGTGACGATGACCTCACTCGGCGGTATTCACCAACC 1083
 Db 2716 AGAATTCATCTCTTCGACAGGTGACGATGACCTCACTCGGCGGTATTCACCAACC 2775
 QY 1084 AGSAGAACGCCATCATCTCCAGGAGATCGTCAAGTACGACCGGAGATGGTGACGAGCGG 1143
 Db 2776 AGSAGAACGCCATCATCTCCAGGAGATCGTCAAGTACGACCGGAGATGGTGACGAGCGG 2835
 QY 1144 AGCTGGGCTCAGCGGTGGGCTCTTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1203
 Db 2836 ACCGCGTCCAGGCTGCTGCTCTGCCACCCCAACCCCAACCCCAACCCCAACCCCAACCC 2895
 QY 1204 CCNATCGGCGGTCGACGAGGCGGCGG 1231
 Db 2896 TGATCCAGGCACCACTGCAGGCTGCGCG 2923

RESULT 7
 US-09-086-436-32
 ; Sequence 32, Application US/09086436
 ; Patent No. 6703485
 ; GENERAL INFORMATION:
 ; APPLICANT: Kandel, Eric R.
 ; APPLICANT: Santoro, Bina
 ; APPLICANT: Bartsch, Dusan
 ; APPLICANT: Siegelbaum, Steven
 ; APPLICANT: Tibbs, Gareth
 ; APPLICANT: Grant, Seth
 ; TITLE OF INVENTION: Brain or Heart Cyclic Nucleotide Gated Ion Channel and
 ; TITLE OF INVENTION: Uses Thereof
 ; FILE REFERENCE: 0575/54806-A

; CURRENT APPLICATION NUMBER: US/09/086,436
 ; CURRENT FILING DATE: 1998-05-28
 ; NUMBER OF SEQ ID NOS: 67
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 32
 ; LENGTH: 1512
 ; TYPE: DNA
 ; ORGANISM: Murine
 ; US-09-086-436-32
 Query Match 65.1%; Score 874.2; DB 4; Length 1512;
 Best Local Similarity 88.9%; Pred. No. 2.2e-170;
 Matches 945; Conservative 0; Mismatches 118; Indels 0; Gaps 0;
 QY 4 TCGCGTTCCAAAGATCTCAGCTCTCGCGGCTGCTGCGGCTCTCAGCGCTCTCAGCGCTGATCCGCT 63
 Db 449 TCGCGTTCCAAAGATCTCAGCTCTGCTGCGGCTGCTGCGGCTATCAGCGCTCATCCGAT 508
 QY 64 ACATCCATCAGTGGGAGGAGATCTTCCACATGACCTATGACTGCGCCAGCGGATGATGA 123
 Db 509 ATATCCACAGTGGGAGGAGATTTTCCACATGACCTAGACCTGGCAAGTGCAGTGATGC 568
 QY 124 GGATCTGCAATCTCATCAGCATGATGCTGCTGCTCTGCGCACTGGGACGCGCTGCTGCACT 183
 Db 569 GCACTGTAACTGATCAGCATGATGCTGCTGCTGCGCACTGGGACGCGTGGCTGCACT 628
 QY 184 TCCTGGTCCCATGCTGCAAGACTTTCGCCAGCGACTGCTGGGTGTCATCAATGGCATGG 243
 Db 629 TCCTGGTCCCATGCTGCAAGACTTTCGCCAGCGACTGCTGGGTGTCATCAATGGCATGG 688
 QY 244 TGAACCACTCGTGGAGCGAGCTCTACTGTTGCGGCTCTTCAAGGCCATGAGCCACATGC 303
 Db 689 TGAACCACTCGTGGAGCGAGCTCTACTGTTGCGGCTCTTCAAGGCCATGAGCCACATGC 748
 QY 304 TGTGATCGGGTACCGCGCGGAGGAGCATGACGAGCATCTGGCTGACCATGC 363
 Db 749 TGTGATCGGGTACCGCGCGGAGGAGCATGACGAGCATCTGGCTGACCATGC 808
 QY 364 TCAGCATGATTTGGGTGCGCACTGCTAGCGCATGTTTATCGGCCACGCGCATGCGCTCA 423
 Db 809 TCAGCATGATCGTAGGCGCCACTGCTATGCCATGTTTCAATTTGGGCAAGCTGCGCTCA 868
 QY 424 TCCAGTCTCGGACTCTCGCGGCGGAGTACCGAGGAGTACAAAGCAGGTGGAGCATG 483
 Db 869 TCCAGTCTCGGACTCTCGCGGCGGAGTACCGAGGAGTACAAAGCAGGTGGAGCATG 928
 QY 484 ACATGTCCTTCCAAAGTTCGAGCTGCTGCTGCGGAGAGTACCAAGCATCTATGAGC 543
 Db 929 ACATGTCCTTCCAAAGTTCGAGCTGCTGCTGCGGAGAGTACCAAGCATCTATGAGC 988
 QY 544 ACCGTTACAGGCGCAAGATGTTTGAAGGAGCAGCATCTCGGCGAGCTCAACGGGCGCC 603
 Db 989 ACCGTTACAGGCGCAAGATGTTTGAAGGAGCAGCATCTCGGCGAGTCAACGGGCGCC 1048
 QY 604 TCGCGGAGGAGTCTGCACTTCACTGCGGAGCTGCTGCGCTCTCAGCGCTGCTGCG 663
 Db 1049 TCGCGGAGGAGTCTGCACTTCACTGCGGAGCTGCTGCGCTCTCAGCGCTGCTGCG 1108
 QY 664 CCAAGCGCGACCCCAACTTTCGTCAGGCGCATGCTGACCAAGCTCAAGTTTCAGAGCTTCC 723
 Db 1109 CCAATGCGAGACCCCAATTTGTCAGCGCATGCTGACAAAGCTCAATTTGAGGCTTCC 1168
 QY 724 AGCGGCTGACTTACATCATTCGCGAGGAGCAGCATCGGGAAGAGATGTAATTCATCCAGC 783
 Db 1169 AGCGTGGAGATTACATCATTCGCGAGGAGGAGCAGCATCGGGAAGAGATGTAATTCATCCAGC 1228
 QY 784 ACGGCGTGTGAGCGTCTCACTAAGGCGCAACAAAGAGATGAAGTGTCCGATGGCTCT 843
 Db 1229 ATGGGGTGTGAGCGTCTCACTAAGGCGCAACAAAGAGATGAAGTGTCCGATGGCTCT 1288
 QY 844 ACTTCGGGAGATCTGCTGCTCAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 903
 Db 1289 ATTTCCGGGAGATCTGCTTGTCTCAGAGGGGCGCGCGGTACCGCCAGCGTGCAGCTGACA 1348

QY 904 CCTACTGCCGCTCTATTTCCTGAGCGTGACCAACTTCAACGAGGTGCTGGAGGATACC 963
Db 1349 CCTACTGTCGCCCTCTACTCACTGAGTGTGGACAAATTTCAACGAGGTGCTGGAGGATACC 1408
QY 964 CCATGATGCGGCGGCCCTTCAGACGCGTGCGCCATCGACCGCCTGGACCGCATCGGCAAGA 1023
Db 1409 CCATGATGCGGCGTGCCCTTTGAGACTGTGGCTATTGACCGGCTAGATCGCATAGGCAAGA 1468
QY 1024 AGAATTCATCTCCTGACAGAGTGCGAGCATGACCTCAATC 1066
Db 1469 AGAATTCATCTCCTGACAGAGTGCGAGCATGATCTCAGTCT 1511

RESULT 8
US-08-997-685A-3
; Sequence 3, Application US/08997685A
; Patent No. 6551821
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Kandel, Eric
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
; FILE REFERENCE: 0575/54806
; CURRENT APPLICATION NUMBER: US/09/97,685A
; CURRENT FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1584
; TYPE: DNA
; ORGANISM: mouse;
US-08-997-685A-3

Query Match 64.9%; Score 871; DB 4; Length 1584;
Best Local Similarity 88.7%; Pred. No. 1e-169;
Matches 943; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 4 TGGCGTTCCACCAAGATCTCAGCTCTCGGCTCTCGGCTCTCAGCGCTGATCGCT 63
Db 449 TGGCGTTCCACCAAGATCTCAGCTCTCGGCTCTCGGCTCTCAGCGCTGATCGCT 508
QY 64 ACATCCATCAGTGGGAGAGATCTTCCACATGACTATGACTCGGCGGCGGCGGTGATGA 123
Db 509 ATATCCACAGTGGGAGAGATTTTCCACATGACTTACGACTTGGCAAGTGCATGATGC 568
QY 124 GGATCTGCAATCTCATCAGCATGATGCTGCTCTGCGCACTGGGAGCGGCTGCTGCAGT 183
Db 569 GCATCTGTAACTCATCAGCATGATGCTGCTCTGCGCACTGGGAGCGGTTGCTGCAGT 628
QY 184 TCCTGGTCCCATGCTGAGGACTTCCGCGCAACTGCTGGTGTCCATCAATGGCATGG 243
Db 629 TCCTGGTCCCATGCTGCAAGACTTCCCGCAGCACTGCTGGTGTCCATCAACCAATGG 688
QY 244 TGAACCACTCTGGAGTGAACCTGCTCTCGCACTCTTCAAGCCCATGAGCCACATGC 303
Db 689 TGAACCACTCTGGAGCGAGCTCTACTGCTTGGCGCTCTTCAAGCCCATGAGCCACATGC 748
QY 304 TGTGATCGGGTACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 363
Db 749 TGTGATCGGGTACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 808
QY 364 TCAGATGATGTTGGTGGCGCACTGCTAGCGCATGTTTCATCGGCGGCGGCGGCGGCGGCGG 423
Db 809 TCAGATGATGTTGGTGGCGCACTGCTAGCGCATGTTTCATCGGCGGCGGCGGCGGCGGCGG 868
QY 424 TCCAGTCTGAGTCTCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 483
Db 869 TCCAGTCTGAGTCTCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 928
QY 484 ACATGCTCTTCCACAAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 543
Db 929 ACATGCTCTTCCACAAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 988

QY 544 ACCGTTACAGGCGAAGATGTTTGAAGGAGCAGCATCTCTGGCGGAGCTCAACGGGCCCC 603
Db 989 ACCGGTACCAAGGAGATGTTCTGATAGGACAGCATCTCTGGGGAACCTCAACGGGCCCC 1048
QY 604 TCGGGAGAGATGCTCAACTTCACTGCGGAGCTGGTGGCTCCATCGCGCTCTGTCG 663
Db 1049 TCGGTGAGAGATGTTGAACCTTCACTGCGGAGCTGGTGGCTCCATCGCGCTCTGTTG 1108
QY 664 CCAAGCCGACCCCAACTTCTGTCAGCGCATGCTGACCAAGCTCAAGTTCGAGGCTCTTC 723
Db 1109 CCAATGACAGCCCAATTTCTGTCAGACCATGCTGACCAAGCTCAAAATTTGAGGCTCTTC 1168
QY 724 AGCGGGTCACTACATCATCCGGAAGGCAACCATCGGGAAGAGATGTATCTTCATCCAGC 783
Db 1169 AGCCTGGAGATTACATCATCCGAGAGGGACCATCGGGAAGAGATGTATCTTCATCCAGC 1228
QY 784 AGCGGTGTCAGCGTCTCACTAAGGGCAACCAAGAGATGAGCTGTCGATGGCTCTCT 843
Db 1229 ATGGGTGTCAGCGTCTCACTAAGGGCAACCAAGAGATGAGCTGTCGATGGCTCTCT 1288
QY 844 ACTTCGGGAGATCTCGCTGCTCACCGGGCGCGCCGACCGGAGCGTGCAGGCTGAC 903
Db 1289 ATTTCCGGGAGATCTCGCTGCTCACAGGGCGCGGCTACGGCCAGGCTGCGAGCTGACA 1348
QY 904 CCTACTGCGGCTCTATTCTGCTGAGCGTGACAACTTCAACGAGGTGCTGGAGGAGTACC 963
Db 1349 CCTACTGTCGCTCTACTCACTGAGTGTGGACAAATTTCAACGAGGTGCTGGAGGAAATACC 1408
QY 964 CCATGATGCGGCGGCTTTCGAGACCGTTCGAGACCGTTCACCGCTTACCGCTTACCG 1023
Db 1409 CCATGATGCGGCGGCTTTCGAGACTGTTGAGACTGTTGAGCTTACCGGCTAGATCGCATAGGCAAGA 1468
QY 1024 AGAATTCATCTCTCTGTCACAAAGTGCAGCATGACCTCAACTC 1066
Db 1469 AGAATTCATCTCTGTCACAAAGTTCAGCATGATCTCAGTCT 1511

RESULT 9
US-09-774-528-317
; Sequence 317, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 802
; CURRENT APPLICATION NUMBER: US/09/774,528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt_fl_genes Version 2.0
; SEQ ID NO 317
; LENGTH: 2976
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)..(2174)
US-09-774-528-317
Query Match 56.0%; Score 751.8; DB 4; Length 2976;

Best Local Similarity 82.6%; Pred. No. 3.5e-145;		Matches 861; Conservative 0; Mismatches 182; Indels 0; Gaps 0;	
QY	4	TGCGCTTACCAAGATCCTCAGCCTCCTGCGGCTGCTGCGCCTCTCACGCTGATCCGCT	63
Db	478	TTGCGCTTACCAAGATCCTAAGCTGCTGAGGCTGCTCGCCTCTCCGCGCTCATCGCT	537
QY	64	ACATCATCAGTGGGAGAGATCTTCCACATGACCTATGACCTTGCGCAGCGGGTGATGA	123
Db	538	ACATACACCAAGTGGGAGAGATCTTTCATATGACCTATGACCTTGCGCAGTGTGTGTTT	597
QY	124	GGATCTGCAATCTCATCAGCATGATGCTGCTGCTGCGCCTGCGCAGTGGGAGGCTGCTGCACT	183
Db	598	GCATCTTCAACCTCATTTGGATGATGCTGCTGCTATGTCACCTGGGATGCTGCTGCACT	657
QY	184	TCTGTGTGCCATGCTGCTGCAAGGATCTCCCGCGCAACTGCTGGGTGTCCATCAATGGCATGG	243
Db	658	TCTGTGTGCCATGCTGCTGCAAGGATCTCCCTCCGACTGCTGGGTCTCCATCAACCATGG	717
QY	244	TGAACCACTCGTGGGAGTGAATCTGTAATCTTTCGCACTCTTCAAGGCGCATGAGCCATGC	303
Db	718	TGAACCACTCGTGGGAGTGAATCTTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	777
QY	304	TGTGATCGGATAGCGCGCGGCGCGGCGGCGGAGGATGACGACATCTGCGTACCATGC	363
Db	778	TGTGATCGGATAGCGCGCGGCGGCGGCGGCGGAGGATGACGACATCTGCGTACCATGC	837
QY	364	TCAGCATGATTTGGGTGGCCACCTGCTAGCGCATGTTTCATCGGCGCACGCGCTGCGCTCA	423
Db	838	TCAGCATGATCGTAGTGCCACATGCTAGCGCATGTTTCATCGGCGCACGCGCTGCGCTCA	897
QY	424	TCAGTGTGATCTCTCGCGCGCGAGTACAGAGAGAGTACAGAGAGAGTACAGAGAGAGT	483
Db	898	TCAGTGTGATCTCTCGCGCGCGAGTACAGAGAGAGTACAGAGAGAGTACAGAGAGAGT	957
QY	484	ACATGCTCTTCCACAGCTGCGAGCTGCTTCCGCGAGAGTACAGAGAGAGTACAGAGAGT	543
Db	958	ACATGCTCTTCCACAGCTGCGAGCTGCTTCCGCGAGAGTACAGAGAGAGTACAGAGAGT	1017
QY	544	ACGCTTACAGGCGCAAGATGTTTGACGAGGACAGCATCTCGGCGGAGCTCAACGCGCGCC	603
Db	1018	ACGCTTACAGGCGCAAGATGTTTCGATGAGGAGAGCATCTCGGCGGAGCTGAGGAGCGC	1077
QY	604	TGCGGAGAGATGCTCAACTTCAACTGCGCGAGAGCTGCTGCGCTCCATGCGCGCTTCCG	663
Db	1078	TTGCGGAGGAGATCATTAATCTTCACTGCTGCGGCGCTGCTGCGCGCGAGTACAGTGGT	1137
QY	664	CCAAAGCGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	723
Db	1138	CCATGCGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1197
QY	724	AGCGGCTGCTACATCATCCGCGAGGACCATCCGCGAGAGAGATGATCTTCACTCAGC	783
Db	1198	AGCGGCGGATCTCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	1257
QY	784	ACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	843
Db	1258	ATGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1317
QY	844	ACTTCGGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	903
Db	1318	ACTTCGGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1377
QY	904	CCTACTGCGGCTCTTATCTGCTGAGGCTGAGCAACTTCAACAGAGGTGCTGAGGAGTACC	963
Db	1378	CCTACTGCGGCTCTTATCTGCTGAGGCTGAGCAACTTCAACAGAGGTGCTGAGGAGTACC	1437
QY	964	CCATGATGCGGCGGCTTTCGAGACCGTGGCCATTCGACCGCTGCGGAGTGGGCAAGA	1023
Db	1438	CCATGATGCGGCGGCTTTCGAGACCGTGGCCATTCGACCGCTGCGGAGTGGGCAAGA	1497
QY	1024	AGAAATTCATCTCTTCGCAAG 1046	

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; Sequence 1, Application US/08997685A			
; Patent No.: 6551821			
; GENERAL INFORMATION:			
; APPLICANT: The Trustees of Columbia University			
; APPLICANT: Kandel, Eric			
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof			
; FILE REFERENCE: 0575/54806			
; CURRENT APPLICATION NUMBER: US/08/997,685A			
; CURRENT FILING DATE: 1997-12-12			
; NUMBER OF SEQ ID NOS: 60			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 1			
; LENGTH: 2733			
; TYPE: DNA			
; ORGANISM: mouse			
US-08-997-685A-1			
Query Match 54.8%; Score 735.2; DB 4; Length 2733;			
Best Local Similarity 78.1%; Pred. No. 8.7e-142;			
Matches 884; Conservative 0; Mismatches 248; Indels 0; Gaps 0;			
QY	4	TGCGCTTACCAAGATCCTCAGCCTCCTGCGGCTGCTGCGCCTCTCACGCTGATCCGCT	63
Db	737	TGAGGTTTACAAAAATCTCAGTCTCTTGGCGTTATTACGCGCTTTCAAAGTTAATCAGAT	796
QY	64	ACATCATCAGTGGGAGGAGATCTTCCACATGACCTATGACCTGCGCAGCGGGTGATGA	123
Db	797	ACATACACCAAGTGGGAGGAGATTTCCACATGACCTATGACCTGCCAGTGTGTGGTGA	856
QY	124	GGATCTGCAATCTCATCAGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	183
Db	857	GGATCTTCAACTCATTTGGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	916
QY	184	TCCTGGTGCCTATGTCAGGACTTCCCGCGCAACTGCTGGGTGCTCAATGGCATGG	243
Db	917	TCCTGGTTCCTGCTGCGGACTTCCACCAAGATTTGCTGGGTCTCTGTAATGAATGG	976
QY	244	TGAACCACTCGTGGAGTGAATGTTACTCTTCCGCACTCTTCAAGGCGCATGAGCCATGC	303
Db	977	TTAATGATTTCTGGGGAACAAATATCTTACGCACTCTTCAAGCTATGATGATCATGC	1036
QY	304	TGTGATCGGCTACCGCGCGGAGGAGCATGACGAGCATGACGACATCTGGCTGACCATGC	363
Db	1037	TGTGATTTGTTATGCGCGCCCAAGCCCTGTGAGCATGCTCTGACCTCTGGATTACCATGC	1096
QY	364	TCAGCATGATTTGGGTGCCACTGCTAGCCCATGTTTCATCGGCGCAGCTGCGCTCA	423
Db	1097	TGAGCATGATTTGGGCGCCACTGCTAGCAATGTTTGTGGCCATGTCACAGCTTTGA	1156
QY	424	TCCAGTCTGCTGACCTCTCGGCGCGGAGTACCAAGAGAGTACCAAGAGTGGAGCATG	483
Db	1157	TCAGTCTTTGAGCTTTCAGAGGAGGAGTATCAAGAGAGTATAGCAAGTAGAGCAAT	1216
QY	484	ACATGCTCTTCCACAAAGCTGCGAGTGTCTCCGCGCAGAAAGTCCACGACTACTATGAGC	543
Db	1217	ACATGCTCTTCCACAAAGTGTACAGCTGACATGCGCGCAGAGATACATGATTAATGAGC	1276
QY	544	ACCGTTACAGGCGAAGATGTTTGAAGGAGACAGCATCTCGGCGGAGCTCAACGGGCCCC	603
Db	1277	ACCGGATACCAAGGCAAGATCTTCGATGAAGAAATATTTCTCAGTGGAGCTTAATGATCTTC	1336
QY	604	TGCGGAGGAGATCTGCAACTTCAACTGCGGAGCTGCTGCGCTCCATCGCGCTGTTCCG	663
Db	1337	TGAGAGAGAAATAGTCAACTTCAACTGCGGAAACTGCTGCTGCTGCTGCTGCTGCTGCTG	1396
QY	664	CCAAAGCGGAGCTTTCGTCAGCGGATGCTGACCAAGCTCAAGTTTCGAGGTCTTCC	723
Db	1397	CTAACGCGGATCCCAATTTGCTGAGCGGATGCTGAGCAAGCTGAGATTTGAGGTGTTCC	1456

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1457 AGCCCGGAGACTATATCATTCGAGAAGGAGCTGTGGGGAAGAAATGTATTTATCCAGC 1516
784 ACAGCGTGGTCAAGCGTCTCACTAAGGGCAACAAAGGAGATGAAGCTGTCCGATGGCTCTCT 843
1517 ACAGTGTGTCTGGGTTATCAACCAAGTCCAGTAAAGAAATGAAGCTGACAGATGGCTCTT 1576
844 ACTTCGGGGAGATCTGCTGCTCACTCCGCGGCGCGCGACGCGAGGCTGCGGGCTGACA 903
1577 ACTTCGGAGAGATATGCTGCTGCTGACCAAGGCGCGGCGCACTGCGAGTGTCCGAGCTGATA 1636
904 CTTACTGCGGCTCTATTCCTGAGGTGACAACTTCAACGAGGTGCTGAGAGAGTACC 963
1637 CTTACTGCTGCTTTACTCCCTTTTCGGTGACAAATTTCAATGAGGCTTGGAGGAATATC 1696
964 CCATGATGCGGCGCGCTTCGAGACGCTGGCCATCGACCGCTCGACCGCATCGGCAAGA 1023
1697 CAATGATGAAGAGCCTTTGAGACAGTTGCTATTCACCGACTCGATCGGATAGGCAAGA 1756
1024 AGAATTCATCTCTGCACAAGGTGAGCATGACCTCAACTCGGGGCTATTCAACCAACC 1083
1757 AAAAACTTATCTCTGAGAGTTCCAGAAAGATCTAAACACTGGTGTGTTTCAACCAACC 1816
1084 AGGAGACGCGCATCATCCAGGAGATGCTCAAGTACGACCGCGAGATGGTSCA 1135
1817 AGGAGACGAGATCCTGAAGCAGATGCTGAAGCATGACCGGAGAGATGGTACA 1868

RESULT 11

US-09-086-436-34

; Sequence 34, Application US/09086436

; Patent No. 6703485

; GENERAL INFORMATION:

; APPLICANT: Kandel, Eric R.

; APPLICANT: Santoro, Bina

; APPLICANT: Bartsch, Dusan

; APPLICANT: Siegelbaum, Steven

; APPLICANT: Tibbs, Gareth

; APPLICANT: Grant, Seth

; TITLE OF INVENTION: Brain or Heart Cyclic Nucleotide Gated Ion Channel and

; TITLE OF INVENTION: Uses Thereof

; FILE REFERENCE: 0575/54806-A

; CURRENT APPLICATION NUMBER: US/09/086,436

; CURRENT FILING DATE: 1998-05-28

; NUMBER OF SEQ ID NOS: 67

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 34

; LENGTH: 1518

; TYPE: DNA

; ORGANISM: Murine

US-09-086-436-34

Query Match 52.6%; Score 706; DB 4; Length 1518;
Best Local Similarity 85.3%; Pred. No. 7.6e-136;
Matches 787; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

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64 ACATCCATCACTGGAGAGATCTTCCACATGACTATGACCTGGCCAGCGCGGTGATGA 123
656 ACATTCATCACTGGGAAGAGATTTTCCACATGACTATGACCTGGCCAGCGCGGTGATC 715
124 GGATCTGAATCTCATCAGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 183
716 GCATCTGAATCTCATGCGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 775
184 TCCTGGTCCCATGCTGCGAGGACTTTCCGCGCAACTGCTGGGTGTCCATCAATGGCATGG 243
776 TCCTAGTCCCATGCTGCGAGGACTTTCCCGCATGACTGCTGGGTGTCCATCAATGGCATGG 835

244 TGAACCACTCGTGGAGTGAATGTACTCTCTCGCACTCTTCAAGGCCATGAGCCACATGC 303
836 TGAATTAATCTCTCTGGGGAAGCAGTATTCTTACGCCCTCTTCAAGGCCATGAGCCACATGC 895
304 TGTGATCGGGTACCGCGCGGAGGAGCATGACGAGCATCTCGGCTGACCATGC 363
896 TGTGATCTGGGTATGAGACGGCAGGCACTGCTAGGCACTGTGACGCTCTGGCTACCATGC 955
364 TCAGCATGATTCGTGGGTGCCACTGCTAGCCATGTTTCAATCGGCCACGCACTGCCCCTCA 423
956 TCAGCATGATTCGTGGGGCCACTGCTATGCCATGTTTCAATCGGCCACGCACTGCCCCTCA 1015
424 TCCAGTTCGTGGACTCTCTCGCGGCCAGTACCAAGAGAAAGTACCAAGAGGTGGAGCAGT 483
1016 TCCAGTTCGTGGACTCTCTCGCGGCCAGTACCAAGAGAAAGTATAAACAGAGGTGGAGCAGT 1075
484 ACATGTCTTCCACAAAGCTGCGAGCTGCTTCCGCGCAGAGATCCACGACTACTATGAGC 543
1076 ACATGTCTTCCACAAAGCTTCCGCGGCCAGTACCAAGAGAAAGTATAAACAGAGGTGGAGCAGT 1135
544 ACCGTTTACCAGGCGCAAGATGTTTGAAGGAGCAGCATCTCTGGCGAGCTCAACGGGCCCC 603
1136 ACCGTTTACCAGGCGCAAGATGTTTGAAGGAGAAAGCATCTCTGGGTGAGTTGAGTGAGCCAC 1195
604 TCGGAGGAGAGATCGTCAACTTCACTGCGGGAAGCTGCTGCGCTCCATGCGGCTGTTCG 663
1196 TTCGAGGAGAGATCACTTAACTGCGGAAGCTGGTGGCATCCATGCCACTGTGTTG 1255
664 CCAACGCGACCCCAACTTCGTCACGCGCATGCTGACCAAGCTCAAGTTCGAGTCTTCC 723
1256 CCAACGCGATCCCAACTTGTGACATCCATGCTGACCAAGTTCGCTTTCGAGGTCTTCC 1315
724 AGCGGCTGACTACATCATCCGGAAGGACCATCCGGAAGAGAGATGTACTTCCATCCAGC 783
1316 AGCCTGGGATTAATCATCTCCGGAAGGACCATCCGGAAGAGAGATGTACTTCCATCCAGC 1375
784 AGCGGCTGCTCAGCGTGTCTCACTAAGGGCAACAAAGGAGATGAAGCTGTCCGATGGCTCT 843
1376 AGCGGCTGCTCAGCGTGTCTCACTAAGGGCAACAAAGGAGACCAAGCTGTGATGGCTCTCT 1435
844 ACTTCGGGAGATCTGCTGCTCACCCTGCGCGCGCGCGCGCGAGGCTGCGGCTGACA 903
1436 ATTTTCGAGAGATCTGCTGCTGACCGCGGCTGCGCGCGCAGCCAGCGTCAGAGCGGATA 1495
904 CTTACTGCGGCTCTATTGCTG 926
1496 CTTATTCCGCTCTTACTCACTG 1518

RESULT 12

US-08-997-685A-5

; Sequence 5, Application US/08997685A

; Patent No. 6551821

; GENERAL INFORMATION:

; APPLICANT: The Trustees of Columbia University

; APPLICANT: Kandel, Eric

; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof

; FILE REFERENCE: 0575/54806

; CURRENT APPLICATION NUMBER: US/08/997,685A

; CURRENT FILING DATE: 1997-12-12

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 1507

; TYPE: DNA

; ORGANISM: mouse;

US-08-997-685A-5

Query Match 51.3%; Score 688.8; DB 4; Length 1507;
Best Local Similarity 85.4%; Pred. No. 2.6e-132;
Matches 779; Conservative 0; Mismatches 132; Indels 1; Gaps 1;

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US-08-937-685A-9
; Sequence 9, Application US/08997685A
; Patent No. 6551821
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Kandel, Eric
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
; FILE REFERENCE: 0575/54806
; CURRENT APPLICATION NUMBER: US/08/997,685A
; CURRENT FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 2263
; TYPE: DNA
; ORGANISM: human
US-08-997-685A-9

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DEPT. T 15

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RESULI 15
US-09-774-528-238
; Sequence 238, Application US/09774528
; Patent NO. 6743619
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; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 802

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; CURRENT APPLICATION NUMBER: US/09/774,528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 238
; LENGTH: 3224
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2673)
US-09-774-528-238

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Query Match      50.7%; Score 680.2; DB 4; Length 3224;
Best Local Similarity 75.0%; Pred. No. 1.8e-130;
Matches 850; Conservative 0; Mismatches 283; Indels 0; Gaps 0;

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DB 830 ACATACATCAATGGGAAGAGATATCCACATGACATATGATCTCGCCAGTGCAGTGA 889

QY 124 GGATCTGCAATCTCATCAGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 183
DB 890 GAAATTTTAAATCTCATCGGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 949

QY 184 TCTGTGTGCCCATGCTGCAGGACTTCCCGCGCAACTGCTGGGTGTCCATCAATG 243
DB 950 TCTTAGTACACTACTGCAAGGACTTCCCAACGAGTTGCTGGGTGTCTTAAATGA 1009

QY 244 TGAACCACTCGTGGAGTGAATCTCTCTGCACTTTCAGGCACTGAGCCACATGC 303
DB 1010 TTAATGATTTTGGGGAAGCAGTATTCATACGCACTTCAAAGCTATGATGATGC 1069

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DB 1190 TCCAGTCTCTGGATTCTTCGAGCGCGCAGTATCAAGAGAAGTATAAGCAAGT 1249

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DB 1250 ACATGTCTATCCATAAGTTACCAGCTGATATGCTGAGAAGATACATGATTAT 1309

QY 544 ACCGTTTACCAGGCAAGATGTTTGAAGGAGCAGCATCTCGCGGAGCTCAACG 603
DB 1310 ACAGATACCAGGCAAAATCTTTGATGAGAAATATCTCAATGAATCAATGATC 1369

QY 604 TCGGGAGGAGATCGTCAACTTCACTGCGGAAGCTGGTGGCTTCCATCGCGCTG 663
DB 1370 TGAGAGAGGAGATAGTCAACTTCACTGTCGGAACCTGGTGGCTACAATGCC 1429

QY 664 CCAAGCCGACCCCAACTTCTGTCAGGCCATGCTGACCAAGCTCAAGTTCGAGG 723
DB 1430 CTAATGCGGATCCTAAATTTTGTGACTGCGCATGCTGAGCAAGTTGAGATT 1489

QY 724 AGCCGGGTGACTACATCATCCGGAAGGCAACCATCGGGAAGAGATGATCTT 783
DB 1490 AACCTGGAGATTATATCATACGAGAAGGAGCCGTGGGTAAAAAATGTTATTT 1549

QY 784 ACGCGGTGGTTCAGCGTGTCTCACTAAGGGCAACAAGGAGATGAAGCTGTC 843
DB 1550 ACGGTGTGTGTGTGTCATTACAAAAATCCAGTAAAGAAATGAAGCTGACAG 1609

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	1194.4	89.0	1790	21	US-10-384-107-11
7	1191.6	88.8	2125	17	US-10-292-798-2011
					Sequence 2, Appli
					Sequence 3, Appli
					Sequence 1720, Ap
					Sequence 40, Appl
					Sequence 40, Appl
					Sequence 11, Appl
					Sequence 2011, Ap

8	1109.2	82.7	1966	15	US-10-017-161-2369	Sequence 2369, Ap
9	1048.6	78.1	3102	14	US-10-067-457-6	Sequence 6, Appli
10	927.2	69.1	4751	18	US-10-311-795-5	Sequence 5, Appli
11	927.2	69.1	5065	14	US-10-067-457-4	Sequence 4, Appli
12	927.2	69.1	5499	18	US-10-276-774-973	Sequence 973, App
13	874.2	65.1	1512	10	US-09-086-436-32	Sequence 32, Appl
14	874.2	65.1	1512	19	US-10-753-991-32	Sequence 32, Appl
15	871	64.9	1584	21	US-10-384-107-3	Sequence 3, Appli
16	753.4	56.1	3952	18	US-10-332-447-57	Sequence 57, Appl
17	751.8	56.0	2325	10	US-09-548-933-2	Sequence 2, Appli
18	751.8	56.0	2325	14	US-10-158-684-9	Sequence 9, Appli
19	751.8	56.0	2325	14	US-10-158-711-9	Sequence 9, Appli
20	751.8	56.0	2376	17	US-10-120-988-317	Sequence 317, App
21	751.8	56.0	3496	18	US-10-311-795-7	Sequence 7, Appli
22	735.2	54.8	2733	21	US-10-384-107-1	Sequence 1, Appli
23	706	52.6	1518	10	US-09-086-436-34	Sequence 34, Appl
24	706	52.6	1518	19	US-10-753-991-34	Sequence 5, Appli
25	688.8	51.3	1507	21	US-10-384-107-5	Sequence 351, App
26	681.8	50.8	2990	18	US-10-287-226-351	Sequence 19, Appl
27	680.2	50.7	1873	16	US-10-296-270-19	Sequence 20, Appl
28	680.2	50.7	1873	16	US-10-296-270-20	Sequence 38, Appl
29	680.2	50.7	2246	10	US-09-086-436-38	Sequence 38, Appl
30	680.2	50.7	2246	19	US-10-753-991-38	Sequence 9, Appli
31	680.2	50.7	2263	21	US-10-384-107-9	Sequence 22, Appl
32	680.2	50.7	2484	16	US-10-296-270-22	Sequence 24, Appl
33	680.2	50.7	2484	16	US-10-296-270-24	Sequence 1, Appli
34	680.2	50.7	2670	18	US-10-311-795-1	Sequence 3, Appli
35	680.2	50.7	2673	14	US-10-158-684-3	Sequence 3, Appli
36	680.2	50.7	2673	14	US-10-158-711-3	Sequence 23, Appl
37	680.2	50.7	2673	16	US-10-296-270-23	Sequence 25, Appl
38	680.2	50.7	2673	16	US-10-296-270-25	Sequence 1, Appli
39	680.2	50.7	2748	21	US-10-466-992-1	Sequence 3, Appli
40	680.2	50.7	2748	21	US-10-466-992-3	Sequence 13, Appl
41	680.2	50.7	2748	21	US-10-466-992-13	Sequence 15, Appl
42	680.2	50.7	2748	21	US-10-466-992-15	Sequence 17, Appl
43	680.2	50.7	2748	21	US-10-466-992-17	Sequence 1, Appli
44	680.2	50.7	2791	16	US-10-296-270-1	Sequence 5, Appli
45	680.2	50.7	2791	16	US-10-296-270-5	

ALIGNMENTS

RESULT 1

US-10-067-457-2
; Sequence 2, Application US/10067457
; Publication No. US20030082513A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharma Deutschland GmbH
; TITLE OF INVENTION: Process for identifying substances which modulate the activity of hyperpolarization-activated cation channels
; FILE REFERENCE: AVE D-2000/A006
; CURRENT APPLICATION NUMBER: US/10/067,457
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US/09/779,587
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 3372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-067-457-2

Query Match	96.6%	Score 1297;	DB 14;	Length 3372;
Best Local Similarity	99.0%	Pred. No. 0;		
Matches 1328;	Conservative	7;	Mismatches	3; Gaps 3;
Qy	4	TGGCTTCACCAAGATCCTCAGCCTCTCGGCTGTGGCCTCTCAGCCTGATCGCT	63	
Db	1012	TGGCTTCACCAAGATCCTCAGCCTCTCGGCTGTGGCCTCTCAGCCTGATCGCT	1071	
Qy	64	ACATCCATCAGTGGGAGGAGATCTTCCACATGACCTATGACCTGGCGCGGTGATGA	123	

Db 1072 ACATCCATCGTGGGAGATCTTCCATGACCTATGACCTGGCCAGCGGGTATGA 1131
Qy 124 GGATCTGCAATCTCATCAGCATGATGCTGCTCTGCGCACTGGGACGGCTCCCTGCAGT 183
Db 1132 GGATCTGCAATCTCATCAGCATGATGCTGCTCTGCGCACTGGGACGGCTCCCTGCAGT 1191
Qy 184 TCTGTGTCCTATGCTGACGAGCTTCCCGGCACTGCTGGGTGCTCCATCAATGGCATGG 243
Db 1192 TCTGTGTCCTATGCTGACGAGCTTCCCGGCACTGCTGGGTGCTCCATCAATGGCATGG 1251
Qy 244 TGAACCACTCGTGGAGTGAATGCTCTCTGCGCACTCTTCAAGGCCATGAGCCACATGC 303
Db 1252 TGAACCACTCGTGGAGTGAATGCTCTCTGCGCACTCTTCAAGGCCATGAGCCACATGC 1311
Qy 304 TGTGATCGGGTACCGCGGACGGCGCCGAGAGCATGACGACATCTGCTGGCTGACCATGC 363
Db 1312 TGTGATCGGGTACCGCGGACGGCGCCGAGAGCATGACGACATCTGCTGACCATGC 1371
Qy 364 TCAGCATGATTTGGGTGCCACTGCTACGCCATGTTTCATCGGCCACGCCACTGCCCTCA 423
Db 1372 TCAGCATGATTTGGGTGCCACCTGCTACGCCATGTTTCATCGGCCACGCCACTGCCCTCA 1431
Qy 424 TCCAGTCGCTGGACTCTCGCGCGCAGTACCAGGAGAAGTACAAAGCAGGTGGAGCAGT 483
Db 1432 TCCAGTCGCTGGACTCTCGCGCGCAGTACCAGGAGAAGTACAAAGCAGGTGGAGCAGT 1491
Qy 484 ACATGTCCTTCCAAAGCTGCCAGTGAATTCGCGCAGAAATCCACGACTACTATGAGC 543
Db 1492 ACATGTCCTTCCAAAGCTGCCAGTGAATTCGCGCAGAAATCCACGACTACTATGAGC 1551
Qy 544 ACCGTTACAGGCAAGATGTTTACGAGGACGAGCATCTGGCGGAGCTCAAGCGGCC 603
Db 1552 ACCGTTACAGGCAAGATGTTTACGAGGACGAGCATCTGGCGGAGCTCAAGCGGCC 1611
Qy 604 TGGGAGGAGATCGTCAACTTCAACTGCGGAGCTGGTGGCTCTCATGCGCGCTGTTCCG 663
Db 1612 TGGGAGGAGATCGTCAACTTCAACTGCGGAGCTGGTGGCTCTCATGCGCGCTGTTCCG 1671
Qy 664 CCAAGCCGACCCAACTTCGTCAAGCCATGCTGACCAAGCTCAAGTTCGAGGCTTCC 723
Db 1672 CCAAGCCGACCCAACTTCGTCAAGCCATGCTGACCAAGCTCAAGTTCGAGGCTTCC 1731
Qy 724 AGCGGGTACTACATCATCTCGGAGGACCATTCGGGAGAGATGATGACTTTCATCCAGC 783
Db 1732 AGCGGGTACTACATCATCTCGGAGGACCATTCGGGAGAGATGATGACTTTCATCCAGC 1791
Qy 784 AGCGGTGCTCAGCGTGTCTCACTAAGGGCAACAAGGAGATGAAGCTGTCGGATGGCTCT 843
Db 1792 AGCGGTGCTCAGCGTGTCTCACTAAGGGCAACAAGGAGATGAAGCTGTCGGATGGCTCT 1851
Qy 844 ACTTCGGGAGATCTGCTGCTCAACCGGGCGCGCAGCGAGCGTGGGGCTGACA 903
Db 1852 ACTTCGGGAGATCTGCTGCTCAACCGGGCGCGCAGCGAGCGTGGGGCTGACA 1911
Qy 904 CTTACTGCGGCTCTATTGCTGAGCGTGGACAACTTCAACGAGGTGCTGGAGGATACC 963
Db 1912 CTTACTGCGGCTCTATTGCTGAGCGTGGACAACTTCAACGAGGTGCTGGAGGATACC 1971
Qy 964 CCATGATGCGGCGGCTTTCAGAGCGTGGCCATCGACCGCTGGACCGCATCGGCAAGA 1023
Db 1972 CCATGATGCGGCGGCTTTCAGAGCGTGGCCATCGACCGCTGGACCGCATCGGCAAGA 2031
Qy 1024 AGAATTCATCTCTGCAAAAGGTGACATGACCTCAACTCGGGCGTATTCAACAAC 1083
Db 2032 AGAATTCATCTCTGCAAAAGGTGACATGACCTCAACTCGGGCGTATTCAACAAC 2091
Qy 1084 AGGAGAACGCCATCATCAGGAGATCGTCAAGTACGACCGGAGATGGTGCAGCGGCC 1143
Db 2092 AGGAGAACGCCATCATCAGGAGATCGTCAAGTACGACCGGAGATGGTGCAGCGGCC 2151
Qy 1144 AGCTGGGCTCAGCGCGTGGGCTCTTCCGCGCGCGCGCGCGCGCGCA-GTCACTCTG 1202

Db 2152 AGCTGGG-TCAGCGGTGGGCTCTTCCGCGCGCGCGCGCGCGCGCGCGCGCTCACCTCG 2210
Qy 1203 GCCATCGCCACGCTGCGCAGCGCGCGCGCATGAGCTTCTGCCCCGCA-GTGGCGCGCGCG 1261
Db 2211 GCCATCGCCACGCTGCGCAGCGCGCGCGCATGAGCTTCTGCCCCGCAAGTGGCGCGCGCG 2270
Qy 1262 CTGCTGGGGCGCGCTGGCGCTCGCGCGCGCTGCTGCGCHGCHGCHGCHGCHGCHGCHGCHG 1321
Db 2271 CTGCTGGGGCGCGCTGGCGCTCGCGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCG 2330
Qy 1322 GCACCTGCHGCHGCHGCHGCHGCHGCHGCHGCHGCHGCHGCHGCHGCHGCHGCHGCHG 1342
Db 2331 GCACCTGCHGCHGCHGCHGCHGCHGCHGCHGCHGCHGCHGCHGCHGCHGCHGCHGCHG 2351

RESULT 2

US-10-311-795-3
; Sequence 3, Application US/10311795
; Publication No. US20040033943A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham plc
; FILE REFERENCE: P32614
; TITLE OF INVENTION: New Use
; CURRENT APPLICATION NUMBER: US/10/311,795
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 3459
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-311-795-3

Query Match 96.5%; Score 1295.4; DB 18; Length 3459;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1327; Conservative 7; Mismatches 4; Indels 3; Gaps 3;

Qy 4 TGGCGTTCACCAAGATCCTCAGCCTCCTGCGGCTGCTGCGGCTCTCAGCGCTGATCCGCT 63
Db 1030 TGGCGTTCACCAAGATCCTCAGCCTCCTGCGGCTGCTGCGGCTCTCAGCGCTGATCCGCT 1089
Qy 64 ACATCCATCAGTGGGAGGAGATCTTCCACATGACCTATGACCTGCGCCAGCGGCTGATGA 123
Db 1090 ACATCCATCAGTGGGAGGAGATCTTCCACATGACCTATGACCTGCGCCAGCGGCTGATGA 1149
Qy 124 GGATCTGCAATCTCATCAGCATGATGCTGCTCTGCGCATGCGGACGGCTGCTGCAGT 183
Db 1150 GGATCTGCAATCTCATCAGCATGATGCTGCTCTGCGCATGCGGACGGCTGCTGCAGT 1209
Qy 184 TCCTGGTCCCATGCTGCGGACTTCCCGCAACTGCTGGGTGCTCCATCAATGGCATGG 243
Db 1210 TCCTGGTCCCATGCTGCGGACTTCCCGCAACTGCTGGGTGCTCCATCAATGGCATGG 1269
Qy 244 TGAACCACTCGTGGAGTGAATGTAATCTCTTCGCACTCTTCAAGGCCATGAGCCACATGC 303
Db 1270 TGAACCACTCGTGGAGTGAATGTAATCTCTTCGCACTCTTCAAGGCCATGAGCCACATGC 1329
Qy 304 TGTGATCGGGTACCGCGCGGAGGCGCCGAGAGATGACGGAATCTGCTGGCTGACCATGC 363
Db 1330 TGTGATCGGGTACCGCGCGGAGGCGCCGAGAGCATGACGACATCTGCTGCTGACCATGC 1389
Qy 364 TCAGCATGATTTGGGTGCCACCTGCTAGCCATGTTTCATGGCCAGCGCACTGCCCTCA 423
Db 1390 TCAGCATGATTTGGGTGCCACCTGCTAGCCATGTTTCATGGCCAGCGCACTGCCCTCA 1449
Qy 424 TCCAGTCTGCTGACTCTCTCGCGCGCCAGTATACAGGAGAAGTACAAGCAGGTGGAGCAGT 483
Db 1450 TCCAGTCTGCTGACTCTCTCGCGCGCCAGTATACAGGAGAAGTACAAGCAGGTGGAGCAGT 1509
Qy 484 ACATGTCCTTCCAAAGCTGCCAGTGAATTCGCGCGCAGAAATCCACGACTACTATGAGC 543
Db 1510 ACATGTCCTTCCAAAGCTGCCAGTGAATTCGCGCGCAGAAATCCACGACTACTATGAGC 1569

544 ACCGTTACAGGCAAGATGTTTTCAGAGGACAGCATCTGGGCGAGCTCAACGGGCCCC 603
1570 ACCGTTACAGGCAAGATGTTTTCAGAGGACAGCATCTGGGCGAGCTCAACGGGCCCC-1629
604 TGGCGGAGGAGATCGTCAACTTCAACTGCGGAGCTGGGCTCATGCCGCTTTTCG 663
1630 TGGCGGAGGAGATCGTCAACTTCAACTGCGGAGCTGGGCTCATGCCGCTTTTCG 1689
664 CCAACGCGACCCCACTTGGTCACGGCCATCTGACCAAGCTCAAGTTTCGAGGCTTTC 723
1690 CCAACGCGACCCCACTTGGTCACGGCCATCTGACCAAGCTCAAGTTTCGAGGCTTTC 1749
724 AGCGGCTGACTACATCATCGCGAAGGACCACTCGGGAAGAGATGATCTTCAATCCAGC 783
1750 AGCGGCTGACTACATCATCGCGAAGGACCACTCGGGAAGAGATGATCTTCAATCCAGC 1809
784 ACGGCGTGGTCAAGTGTCTCACTAAGGGCAACAGGAGATGAAGCTGTCCGATGGTCTCT 843
1810 ACGGCGTGGTCAAGTGTCTCACTAAGGGCAACAGGAGATGAAGCTGTCCGATGGTCTCT 1869
844 ACTTGGGAGAGATCTGCTGCTCACTACCGGGGCGCGCAGCGAGGCTGGGCTGACA 903
1870 ACTTGGGAGAGATCTGCTGCTCACTACCGGGGCGCGCAGCGAGGCTGGGCTGACA 1929
904 CCTACTGCCGCTCTATTTCGCTGAGCGTGGACAACTTCAACGAGGTGCTGGAGAGTACC 963
1930 CCTACTGCCGCTCTATTTCGCTGAGCGTGGACAACTTCAACGAGGTGCTGGAGAGTACC 1989
964 CCATGATGCGGCGGCTTTCAGACGGTGGCCATCGACCGCTTGGACCGCATCGGCAAGA 1023
1990 CCATGATGCGGCGGCTTTCAGACGGTGGCCATCGACCGCTTGGACCGCATCGGCAAGA 2049
1024 AGAATTCATCTCTGTCACAAAGTGCAGATGACCTCAACTGGGGTATTCAACAACC 1083
2050 AGAATTCATCTCTGTCACAAAGTGCAGATGACCTCAACTGGGGTATTCAACAACC 2109
1084 AGGAGACGCATCATCAGAGATCGTCAAGTACGACCGGAGATGGTGCAGCGCCG 1143
2110 AGGAGACGCATCATCAGAGATCGTCAAGTACGACCGGAGATGGTGCAGCGCCG 2169
1144 AGCTGGGCTCAGCGCTGGGCTCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1202
2170 AGCTGGG-TCAGCGCTGGGCTCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2228
1203 GCCATGCCACGCTGCAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1261
2229 GCCATGCCACGCTGCAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2288
1262 CTCGTGGGCGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 1321
2289 CTCGTGGGCGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 2348
1322 GCACCTGCHGCGCTTCAACC 1342
2349 GCACCTGCHGCGCTTCAACC 2369

RESULT 3
US-10-756-149-1720
; Sequence 1720, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziiz, Natasha
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1720
; LENGTH: 3459

TYPE: DNA
ORGANISM: Homo Sapiens
US-10-756-149-1720
Query Match 96.5%; Score 1295.4; DB 22; Length 3459;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1327; Conservative 7; Mismatches 4; Indels 3; Gaps 3;
4 TCGCGTTCAACCAAGATCTCTCAGCTCTCTGGCGCTCTGGCGCTCTCAGCGCTGATCCGCT 63
1030 TCGCGTTCAACCAAGATCTCTCAGCTCTCTGGCGCTCTGGCGCTCTCAGCGCTGATCCGCT 1089
64 ACATCCATCAGTGGAGAGATCTTCCATGACATGACCTATGACCTGGCAGCGGATGATCA 123
1090 ACATCCATCAGTGGAGAGATCTTCCATGACCTATGACCTGGCAGCGGATGATCA 1149
124 GGATCTGCATCTCATCAGCATGATCTGCTCTGCGACCTGGGAGCGCTGCTGCACT 183
1150 GGATCTGCATCTCATCAGCATGATCTGCTCTGCGACCTGGGAGCGCTGCTGCACT 1209
184 TCCTGTGCTCCATGCTGCGAGGACTTCCCGCGCAACTGCTGGGTGTCATCAATGGCATGG 243
1210 TCCTGTGCTCATGCTGCGAGGACTTCCCGCGCAACTGCTGGGTGTCATCAATGGCATGG 1269
244 TGAACCACTCTGTGGAGTGAATCTGTACTCTTCCGCACTCTTCAAGGCGCATGAGCACA 303
1270 TGAACCACTCTGTGGAGTGAATCTGTACTCTTCCGCACTCTTCAAGGCGCATGAGCACA 1329
304 TGTGATTCGGGTACCGCGCGGAGGCGCGGAGAGCATGACGACATCTGGCTGACCATGC 363
1330 TGTGATTCGGGTACCGCGCGGAGGCGCGGAGAGCATGACGACATCTGGCTGACCATGC 1389
364 TCAGCATGATCTGGGTGCGCACTGCTAGCGCATGTTCACTCGGCCACGCGACCTGCGCTCA 423
1390 TCAGCATGATCTGGGTGCGCACTGCTAGCGCATGTTCACTCGGCCACGCGACCTGCGCTCA 1449
424 TCAGTCTGCTGAGCTCTCTCGCGCGCAGTACAGGAGAGTACAAGAGAGTGGAGCAGT 483
1450 TCAGTCTGCTGAGCTCTCTCGCGCGCAGTACAGGAGAGTACAAGAGAGTGGAGCAGT 1509
484 ACATGTCCTTCCAAAGCTGCCAGCTGACTTCCGCGCAGAGATCCACGACTACTATGAGC 543
1510 ACATGTCCTTCCAAAGCTGCCAGCTGACTTCCGCGCAGAGATCCACGACTACTATGAGC 1569
544 ACCTGTTACAGGCAAGATGTTTTCAGAGGACAGCATCTGGCGGAGCTCAACGGGCCCC 603
1570 ACCTGTTACAGGCAAGATGTTTTCAGAGGACAGCATCTGGCGGAGCTCAACGGGCCCC 1629
604 TGGCGGAGGAGATCGTCAACTTCAACTGCGGAGCTGGGCTCCATGCGCGCTGTTTCG 663
1630 TGGCGGAGGAGATCGTCAACTTCAACTGCGGAGCTGGGCTCCATGCGCGCTGTTTCG 1689
664 CCAACGCGACCCCACTTGGTCACGGCCATCTGACCAAGCTCAAGTTTCGAGGCTTTC 723
1690 CCAACGCGACCCCACTTGGTCACGGCCATCTGACCAAGCTCAAGTTTCGAGGCTTTC 1749
724 AGCGGCTGACTACATCATCGCGAAGGACCACTCGGGAAGAGATGATCTTCAATCCAGC 783
1750 AGCGGCTGACTACATCATCGCGAAGGACCACTCGGGAAGAGATGATCTTCAATCCAGC 1809
784 ACGGCGTGGTCAAGTGTCTCACTAAGGGCAACAGGAGATGAAGCTGTCCGATGGTCTCT 843
1810 ACGGCGTGGTCAAGTGTCTCACTAAGGGCAACAGGAGATGAAGCTGTCCGATGGTCTCT 1869
844 ACTTGGGAGAGATCTGCTGCTCACTACCGGGGCGCGCAGCGAGGCTGGGCTGACA 903
1870 ACTTGGGAGAGATCTGCTGCTCACTACCGGGGCGCGCAGCGAGGCTGGGCTGACA 1929
904 CCTACTGCCGCTCTATTTCGCTGAGCGTGGACAACTTCAACGAGGTGCTGGAGAGTACC 963
1930 CCTACTGCCGCTCTATTTCGCTGAGCGTGGACAACTTCAACGAGGTGCTGGAGAGTACC 1989
964 CCATGATGCGGCGGCTTTCAGACGGTGGCCATCGACCGCTTGGAGCGCATCGGCAAGA 1023

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Db      1990  CCATGATGGGGCGGCTTCGAGACGGTGGCCATGACCGCTGGACCCGATCGGCAAGA 2049
QY      1024  AGAATTCATCTCTCTGCAACAAGTGTGACATGACCTCAACTCGGCGTATTCAACAACC 1083
Db      2050  AGAATTCATCTCTCTGCAACAAGTGTGACATGACCTCAACTCGGCGTATTCAACAACC 2109
QY      1084  AGGAGAACCCATCATCTCAGGAGATCGTCAAGTACGACCGGAGATGGTGCAGCGCGG 1143
Db      2110  AGGAGAACCCATCATCTCAGGAGATCGTCAAGTACGACCGGAGATGGTGCAGCGCGG 2169
QY      1144  AGCTGGGCTCAGCGGTGGGCTCTTCCCGCGCGCGCGCGCGCGCGCGCA-GTCAACCTCG 1202
Db      2170  AGCTGGG-TCAGCGCGTGGGCTCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCG 2228
QY      1203  GCCATCGCCACGCTGAGCGGCGGCGCATGAGCTTCTGCCCGCA-GTGGCGGCGG 1261
Db      2229  GCCATCGCCACGCTGAGCGGCGGCGCATGAGCTTCTGCCCGCGAGGTGGCGGCGG 2288
QY      1262  CTCGTGGGCGGCTGGCGCTCGGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1321
Db      2289  CTCGTGGGCGGCTGGCGCTCGGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2348
QY      1322  GCACCTGCHGCNCCCTCAACC 1342
Db      2349  GCACCTGCGCGCGCTCAACC 2369

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RESULT 4
US-09-086-436-40
; Sequence 40, Application US/09086436
; Publication No. US2003011898A1
; GENERAL INFORMATION:
; APPLICANT: Santoro, Bina
; APPLICANT: Bartsch, Dusan
; APPLICANT: Siegelbaum, Steven
; APPLICANT: Tibbs, Gareth
; APPLICANT: Grant, Seth
; TITLE OF INVENTION: Brain or Heart Cyclic Nucleotide Gated Ion Channel and
; FILE REFERENCE: 0575/54806-A
; CURRENT APPLICATION NUMBER: US/09/086,436
; CURRENT FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 1792
; TYPE: DNA
; ORGANISM: Human
US-09-086-436-40

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Query Match      89.9%; Score 1207; DB 10; Length 1792;
Best Local Similarity 99.0%; Pred. No. 9.2e-311;
Matches 1235; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

QY      4    TGGCTTCCACCAAGATCTCAGCCTCTCTGGGCTGTCTGGGCTCTCAACCTGATCGCT 63
Db      541  TGGCTTCCACCAAAATCTCTCAGCCTCTCTGGGCTGTCTGGGCTCTCAACCTGATCGCT 600
QY      64    ACATCCATCAGTGGGAGGATCTTCCACATGACCTATGACCTGGCGGCGGTGATGA 123
Db      601  ACATCCATCAGTGGGAGGATCTTCCACATGACCTATGACCTGGCGGCGGTGATGA 660
QY      124  GGATCTGCAATCTCATCAGCATGATCTGCTCTGCGCACTGGGAGCGGCTGCGAGT 183
Db      661  GGATCTGCAATCTCATCAGCATGATCTGCTCTGCGCACTGGGAGCGGCTGCGAGT 720
QY      184  TCTGTGTGCCATGTCTGAGGACTTCCCGCGCAACTGCTGGGTGTCATCAATGGCATGG 243
Db      721  TCTGTGTGCTATGTCTGAGGACTTCCCGCGCAACTGCTGGGTGTCATCAATGGCATGG 780
QY      244  TGAACCACTCGTGGAGTGAAGTACTCTTCCGCACTCTTCAAGGCGCATGAGCCATGCG 303

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RESULT 5
US-10-753-991-40
; Sequence 40, Application US/10753991
; Publication No. US2004014242A1
; GENERAL INFORMATION:

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Db      781  TGAACCACTCGTGGAGTGAATGTACTCTTTCGCACTCTTCAAGGCGCATGAGCCATGCG 840
QY      304  TGTGATCGGTAFCGCGCGGAGGAGCATGACGGAATCTTGGGTGACATGCG 363
Db      841  TGTGATCGGTAFCGCGCGGAGGAGGAGCATGACGGAATCTTGGGTGACATGCG 900
QY      364  TCAGCATGATTTGTGGGTGCGACCTGTACGCGCATGTTTTCATGGGCCACGCCATGCGCTCA 423
Db      901  TCAGCATGATTTGTGGGTGCGACCTGTACGCGCATGTTTTCATGGGCCACGCCATGCGCTCA 960
QY      424  TCCAGTCTCGTGGACTCTCTCGCGGCGCAGTACCAAGGAGAGTACCAAGGAGGAGTGAAGT 483
Db      961  TCCAGTCTCGTGGACTCTCTCGCGGCGCAGTACCAAGGAGAGTACCAAGGAGGAGTGAAGT 1020
QY      484  ACATGTCTTCCACAAGTGTGCGAGTGTCTTCCGCGCAGAGATCCACGATCTATGAGC 543
Db      1021  ACATGTCTTCCACAAGTGTGCGAGTGTCTTCCGCGCAGAGATCCACGATCTATGAGC 1080
QY      544  ACCGTTCACAGGCGCAAGATGTTTACGAGGAGACAGCATCTTGGGCGAGCTCAACGGGCGCC 603
Db      1081  ACCGTTCACAGGCGCAAGATGTTTACGAGGAGACAGCATCTTGGGCGAGCTCAACGGGCGCC 1140
QY      604  TGGCGGAGGAGATCGTCAACTTCAACTGCGGAGAGTGGTGGCTTCCATGCGGCTGTTGG 663
Db      1141  TGGCGGAGGAGATCGTCAACTTCAACTGCGGAGAGTGGTGGCTTCCATGCGGCTGTTGG 1200
QY      664  CCAACGCGGAGAGTGTCTGTCAGGCGCATGTCACCAAGCTCAAGTTCGAGGCTTTC 723
Db      1201  CCAACGCGGAGAGTGTCTGTCAGGCGCATGTCACCAAGCTCAAGTTCGAGGCTTTC 1260
QY      724  AGCGGGGTGACTACATCATCTCGCGAGGAGCATCTCGGAGAGAGTGTACTTCATCCAGC 783
Db      1261  AGCGGGGTGACTACATCATCTCGCGAGGAGCATCTCGGAGAGAGTGTACTTCATCCAGC 1320
QY      784  AGCGGTGTGTGAGGTGTCTCACTAAGGCGCAACAGGAGATGAAGTGTCCGATGCTCTCT 843
Db      1321  AGCGGTGTGTGAGGTGTCTCACTAAGGCGCAACAGGAGATGAAGTGTCCGATGCTCTCT 1380
QY      844  ACTTCGGGAGATGTGCTGTCTCACTCGGCGCGCGCGCGCGCGAGCTGCGGCTGACA 903
Db      1381  ACTTCGGGAGATGTGCTGTCTCACTCGGCGCGCGCGCGCGCGAGCTGCGGCTGACA 1440
QY      904  CCTACTCGCGCTCTATTTCGCTGAGCGTGGACACTTCAACGAGGTGTGAGGAGTACC 963
Db      1441  CCTACTCGCGCTCTATTTCGCTGAGCGTGGACACTTCAACGAGGTGTGAGGAGTACC 1500
QY      964  CCATGATCGCGCGCGCTTTCGAGAGCGTGGCCATCGACCGCTGACCGCATCGGCAAGA 1023
Db      1501  CCATGATCGCGCGCGCTTTCGAGAGCGTGGCCATCGACCGCTGACCGCATCGGCAAGA 1560
QY      1024  AGAATTCATCTCTCTGCAACAAGTGTGAGCATGACCTCAACTCGGCGGTATTCAACAACC 1083
Db      1561  AGAATTCATCTCTCTGCAACAAGTGTGAGCATGACCTCAACTCGGCGGTATTCAACAACC 1620
QY      1084  AGGAGAACCCATCATCTCAGGAGATCTCAAGTACGCGGAGATGGTGCAGGAGCGCG 1143
Db      1621  AGGAGAACCCATCATCTCAGGAGATCTCAAGTACGCGGAGATGGTGCAGGAGCGCG 1680
QY      1144  AGCTGGGCTCAGCGGTGGGCTCTTTCGCGCGCGCGCGCGCGCGCGCGCA-GTCACTCG 1202
Db      1681  AGCTGGG-TCAGCGGTGGGCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCTACTTCG 1739
QY      1203  GCCATCGCCACGCTGACGAGCGCGCGCGCATGAGCTTCTGCGCGCGAG 1250
Db      1740  GCCATCGCCACGCTGACGAGCGCGCGCGCATGAGCTTCTGCGCGCGAG 1787

```

APPLICANT: Kandel, Eric R.
APPLICANT: Santoro, Bina
APPLICANT: Bartsch, Dusan
APPLICANT: Siegelbaum, Steven
APPLICANT: Tibbs, Gareth
APPLICANT: Grant, Seth
TITLE OF INVENTION: Brain or Heart Cyclic Nucleotide Gated Ion Channel and
FILE REFERENCE: 0575/54806-A
CURRENT APPLICATION NUMBER: US/10/753,991
CURRENT FILING DATE: 2004-01-07
EARLIER APPLICATION NUMBER: 09/086,436
EARLIER FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn ver. 2.1
SEQ ID NO 40
LENGTH: 1792
TYPE: DNA
ORGANISM: Human
US-10-753-991-40

Query Match 89.9%; Score 1207; DB 19; Length 1792;
Best Local Similarity 99.0%; Pred. No. 9.2e-311;
Matches 1235; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

QY 4 TGGCTTACCAAGATCCTCAGCCTCTCGGGTGTGCTGCGCTCTCAGCGCTGATCGCT 63
DB 541 TGGCTTACCAAAATCCTCAGCCTCTCGGGTGTGCTGCGCTCTCAGCGCTGATCGCT 600
QY 64 ACATCCATCAGTGGAGAGATCTTCCATGACCTATGACCTGGCCAGCGCGGTGATGA 123
DB 601 ACATCCATCAGTGGAGAGATCTTCCATGACCTATGACCTGGCCAGCGCGGTGATGA 660
QY 124 GGATCTGCAATCTCATCAGCATGATGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 183
DB 661 GGATCTGCAATCTCATCAGCATGATGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 184 TCCTGGTCCCATGCTCTCAGGATCTTCCGCGCACTGCTGGGTGTCCATCAATGGCATGG 243
DB 721 TCCTGGTCCCATGCTCTCAGGATCTTCCGCGCACTGCTGGGTGTCCATCAATGGCATGG 780
QY 244 TGAACCACTCGTGAGTGAATGCTGCTTCTGCACTCTTCAAGGCCATCAGGCCATGTC 303
DB 781 TGAACCACTCGTGAGTGAATGCTGCTTCTGCACTCTTCAAGGCCATCAGGCCATGTC 840
QY 304 TGTGCATCGGTACGGCCGGCAGCGCCGAGAGCATGACGAGCATCTGGCTGACCATGC 363
DB 841 TGTGCATCGGTACGGCCGGCAGCGCCGAGAGCATGACGAGCATCTGGCTGACCATGC 900
QY 364 TCAGCATGATGGGTGCCACCTGCTACGCCATGTTTCATCGGCCACGCCACCTGCCCTCA 423
DB 901 TCAGCATGATGGGTGCCACCTGCTACGCCATGTTTCATCGGCCACGCCACCTGCCCTCA 960
QY 424 TCCAGTCTGAGTCTCTCGGGGCGCAGTACAGGAGAGTCAAGCAGTGGAGCAGT 483
DB 961 TCCAGTCTGAGTCTCTCGGGGCGCAGTACAGGAGAGTCAAGCAGTGGAGCAGT 1020
QY 484 ACATGTCTCTCCACAAGTGCAGTGAATTCGCCAGAGATCCAGCATCTATGAGC 543
DB 1021 ACATGTCTCTCCACAAGTGCAGTGAATTCGCCAGAGATCCAGCATCTATGAGC 1080
QY 544 ACCGTTACAGGCGAAGATGTTTGAAGGAGCAGCATCTGGGGAGCTCAAGGGCCCC 603
DB 1081 ACCGTTACAGGCGAAGATGTTTGAAGGAGCAGCATCTGGGGAGCTCAAGGGCCCC 1140
QY 604 TGGCGGAGGATCGTCAACTTCAACTTCCAGGAGCTGGTGGCTTCCATGCGCTGTTCG 663
DB 1141 TGGCGGAGGATCGTCAACTTCAACTTCCAGGAGCTGGTGGCTTCCATGCGCTGTTCG 1200
QY 664 CCAACGCGGAGCTTCTGTCAGCGCATGCTGACCAAGCTCAAGTTCGAGGTCTTCC 723
DB 1201 CCAACGCGGAGCTTCTGTCAGCGCATGCTGACCAAGCTCAAGTTCGAGGTCTTCC 1260

QY 724 AGCGGGTGACTATCATATCCGCGAAGGACCATCGGGAAGAGATGATCTTATCCAGC 783
DB 1261 AGCGGGTGACTATCATATCCGCGAAGGACCATCGGGAAGAGATGATCTTATCCAGC 1320
QY 784 ACGGGGTGTGAGCGTGTCTACTAAGGGGCAAGAGATGAAGTGTCCGATGGCTCT 843
DB 1321 ACGGGGTGTGAGCGTGTCTACTAAGGGGCAAGAGATGAAGTGTCCGATGGCTCT 1380
QY 844 ACTTCGGGAGATCTGCTCTGCTCAGCCGGGGCGCGCACGCGGAGCGTGGGGCTGACA 903
DB 1381 ACTTCGGGAGATCTGCTCTGCTCAGCCGGGGCGCGCACGCGGAGCGTGGGGCTGACA 1440
QY 904 CCTACTGCGCTCTTATTCGCTGAGCGTGAACAATTCACAGAGTGTGGAGGATGAC 963
DB 1441 CCTACTGCGCTCTTATTCGCTGAGCGTGAACAATTCACAGAGTGTGGAGGATGAC 1500
QY 964 CCATGATGCGCGCGCTTCGAGAGCGGTGGCCATGACCGCTGACCCGCGCAAG 1023
DB 1501 CCATGATGCGCGCGCTTCGAGAGCGGTGGCCATGACCGCTGACCCGCGCAAG 1560
QY 1024 AGAATTCATCTCTCTGCAACAAGGTGACGATGACCTCAACTCGGGCGTATTCACAACC 1083
DB 1561 AGAATTCATCTCTCTGCAACAAGGTGACGATGACCTCAACTCGGGCGTATTCACAACC 1620
QY 1084 AGGAGAACCCATCATCCAGGAGATGCTCAAGTACGACCGCGAGATGTTGACGAGCGG 1143
DB 1621 AGGAGAACCCATCATCCAGGAGATGCTCAAGTACGACCGCGAGATGTTGACGAGCGG 1680
QY 1144 AGCTGGCTCAGCGGTGGCGCTCTTCCGCGCGCGCGCGCGCGCGCGCA-GTCACTCG 1202
DB 1681 AGCTGGG-TCAGCGCGTGGCGCTTTTTCGCGCGCGCGCGCGCGCGCGCGCACTTCG 1739
QY 1203 GCATCGCCACGCTGCGAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 1250
DB 1740 GCATCGCCACGCTGCGAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 1787

RESULT 6

US-10-384-107-11
Sequence 11, Application US/10384107
Publication No. US20050003477A1
GENERAL INFORMATION:
APPLICANT: The Trustees of Columbia University
APPLICANT: Kandel, Eric R.
APPLICANT: Santoro, Bina
APPLICANT: Bartsch, Dusan
APPLICANT: Siegelbaum, Steven
APPLICANT: Tibbs, Gareth
APPLICANT: Grant, Seth
TITLE OF INVENTION: Pacemaker Channel Proteins and Uses Thereof
FILE REFERENCE: 0575/54806-B
CURRENT APPLICATION NUMBER: US/10/384,107
CURRENT FILING DATE: 2003-03-06
PRIOR APPLICATION NUMBER: 08/997,685
PRIOR FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 1790
TYPE: DNA
ORGANISM: human;
US-10-384-107-11

Query Match 89.0%; Score 1194.4; DB 21; Length 1790;
Best Local Similarity 98.9%; Pred. No. 2.1e-307;
Matches 1234; Conservative 0; Mismatches 11; Indels 3; Gaps 3;

QY 4 TGGCTTACCAAGATCCTCAGCCTCTCGGGTGTGCTGCGCTCTTCAAGCTGATCGCT 63
DB 540 TGGCTTACCAAAATCCTCAGCCTCTCGGGTGTGCTGCGCTCTCAGCGCTGATCGCT 599
QY 64 ACATCCATCAGTGGGAGAGATCTTCCATGACCTATGACCTTGGCGAGCGCGGTGATGA 123

Db 600 ACATCCATCAGTGGGAGGAGATCTTCCACATGACCTATGACCTGGCCAGCGGCGGTGATGA 659
Qy 124 GGATCTGCAATCTCATCAGCATGATGCTGCTGTGCGCACTGGGACGGCTGCCGTGCAGT 183
Db 660 GGATCTGCAATCTCATCAGCATGATGCTGCTGTGCGCACTGGGACGGCTGCCGTGCAGT 719
Qy 184 TCTGTGTCCTGCTGCGAGGACTTCCCGGCACTGCTGGGTGTCCATCAATGGCATGG 243
Db 720 TCTGTGTCCTATGCTGCGAGGACTTCCCGGCACTGCTGGGTGTCCATCAATGGCATGG 779
Qy 244 TGAACCACTCTGTGGAGTGAATGCTACTCTCTTGCACCTTCAAGGGCCATGAGCCACATGC 303
Db 780 TGAACCACTCTGTGGAGTGAATGCTACTCTCTTGCACCTTCAAGGGCCATGAGCCACATGC 839
Qy 304 TGTGTCATCGGGTACGGCCGCGCAGGCGCCGAGAGCATGACGCAATCTGGCTGACCATGC 363
Db 840 TGTGTCATCGGGTACGGCCGCGCAGGCGCCGAAAGCATGACGACATCTGGCTGACCATGC 899
Qy 364 TCAGCATGATTGGGTGCGCACCTGTACGCCATGTTTCATCGGCCACGCACTGCCCTCA 423
Db 900 TCAGCATGATTGGGTGCGCACCTGTACGCCATGTTTCATCGGCCACGCACTGCCCTCA 959
Qy 424 TCCAGTCTGCTGACTCTCGCGCGCAGTACCAGGAGAACTACAGAGAGTGGAGCAGT 483
Db 960 TCCAGTCTGCTGACTCTCGCGCGCAGTACCAGGAGAACTACAGAGAGTGGAGCAGT 1019
Qy 484 ACATGTCCTTCCACAAAGCTGCCAGCTGACTTCGCCAGAGATCCACGACTACTATGAGC 543
Db 1020 ACATGTCCTTCCACAAAGCTGCCAGCTGACTTCGCCAGAGATCCACGACTACTATGAGC 1079
Qy 544 ACCGTTACCGGCAAGATGTTTGACGAGGACGATCTTGGCGAGCTCAACGGGCCCC 603
Db 1080 ACCGTTACCGGCAAGATGTTTGACGAGGACGATCTTGGCGAGCTCAACGGGCCCC 1139
Qy 604 TCGCGGAGAGATCGTCAACTCACTGCGGAGCTGGTGGCTCCATGCGCTGTTCCG 663
Db 1140 TCGCGGAGAGATCGTCAACTCACTGCGGAGCTGGTGGCTCCATGCGCTGTTCCG 1199
Qy 664 CCACGCCGACCCCAACTTCGTCA CGGCCATGCTGACCAAGCTCAAGTTCGAGGTCTTCC 723
Db 1200 CCACGCCGACCCCAACTTCGTCA CGGCCATGCTGACCAAGCTCAAGTTCGAGGTCTTCC 1259
Qy 724 AGCCGGGTGACTATCATCTCCGGAAGGACCACTCCGGAAGAGATGTAATTCATCCAGC 783
Db 1260 AGCCGGGTGACTATCATCTCCGGAAGGACCACTCCGGAAGAGATGTAATTCATCCAGC 1319
Qy 784 AGCGGTGTGTGAGCGTGTCACTAAGGCGCAACAGGAGATGAAGCTGCCGATGGCTCT 843
Db 1320 AGCGGTGTGTGAGCGTGTCACTAAGGCGCAACAGGAGATGAAGCTGCCGATGGCTCT 1379
Qy 844 ACTTCGGGGAGATCTGCTGCTCA CCGGGGCGCCGCA CGGCGAGCGTGGCGGCTGACA 903
Db 1380 ACTTCGGGGAGATCTGCTGCTCA CCGGGGCGCCGCA CGGCGAGCGTGGCGGCTGACA 1438
Qy 904 CTTACTGCGCCCTCTATTGCTGAGCGTGGA CAACTTCAACGAGGTGCTGGAGAGTACC 963
Db 1439 CTTACTGCGCCCTCTATTGCTGAGCGTGGA CAACTTCAACGAGGTGCTGGAGAGTACC 1498
Qy 964 CCATGATGGGGCGCGCTTTCGAGACGTGGCCATCGACCGCTTGGACCGCATCGGCAAGA 1023
Db 1499 CCATGATGGGGCGCGCTTTCGAGACGTGGCCATCGACCGCTTGGACCGCATCGGCAAGA 1558
Qy 1024 AGAATTCATCTCTCTGCA CAAAGGTGACGATGACCTCAACTCGGGCGTATTCAACAACC 1083
Db 1559 AGAATTCATCTCTCTGCA CAAAGGTGACGATGACCTCAACTCGGGCGTATTCAACAACC 1618
Qy 1084 AGAGAAACCGCATCTCAGAGATCGTCAAGTACGACCGCGAGATGGTGCAGAGCGCG 1143
Db 1619 AGAGAAACCGCATCTCAGAGAGATCGTCAAGTACGACCGCGAGATGGTGCAGAGCGCG 1678
Qy 1144 AGCTGGGCTCAGCGCGTGGGCTCTTCCGCGCGCGCGCGCGCGCGCA -GTCACTCG 1202
Db 1679 AGCTGGG -TCAGGCGGTGGGCTTTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCTCACTTCG 1737

Qy 1203 GCCATCGCCACGCTGCACGACGCGCGCCCATGAGCTTCTGCCCGCAG 1250
Db 1738 GCCATCGCCACGCTGCACGACGCGCGCCCATGAGCTTCTGCCCGCAG 1785

RESULT 7

US-10-292-798-2011
; Sequence 2011, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABRURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2011
; LENGTH: 2125
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: source
; FEATURE:
; LOCATION: (1)..(2125)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1724)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1767)..(1925)
US-10-292-798-2011

Query Match 88.8%; Score 1191.6; DB 17; Length 2125;
Best Local Similarity 95.2%; Pred. No. 1.2e-306;
Matches 1276; Conservative 7; Mismatches 47; Indels 10; Gaps 5;

Qy 4 TCGCTTCCACCAAGATCTTCAGCCTCCTGCGCTGCTGCGCTCTTCACGCGCTGATCCGCT 63
Db 688 TCGCTTCCACCAAGATCTTCAGCCTCCTGCGCTGCTGCGCTCTTCACGCGCTGATCCGCT 747
Qy 64 ACATCCATCAGTGGGAGGAGATCTTCCACATGACCTATGACCTGGCCAGCGGCGGTGATGA 123
Db 748 ACATCCATCAGTGGGAGGAGATCTTCCACATGACCTATGACCTGGCCAGCGGCGGTGATGC 807
Qy 124 GGATCTGCAATCTCATCAGCATGATGCTGCTGCTGCGACCTGGGACGCGCTGCCCTGCAGT 183
Db 808 GGTTCTGCAACCTCATCAGTATGATGCTGCTGCTGCGACCTGGGATGGCTGCCCTGCAGT 867
Qy 184 TCTGTGTCCTCATGCTGCGAGGACTTCCCGCGCACTGCTGGGTGTCCATCAATGGCATGG 243
Db 868 TCTGTGTCCTCATGCTGCGAGGACTTCCCGTGCACTGCTGGGTGTCCATCAATGGCATGG 927
Qy 244 TGAACCACTCTGTGGAGTGAATGTAATCTTCTGCGACTCTTCAAGGCCATGAGCCACATGC 303
Db 928 TGAACCACTCTGTGGAGTGAATGTAATCTTCTGCGACTCTTCAAGGCCATGAGCCACATGC 987
Qy 304 TGTGATCGGGTACCGCGCGGCGCGGAGAGCATGACGACATCTGGCTGACCATGC 363
Db 988 TGTGATTTGGGTATGGCGCGGCGCGGAGAGCATGACGACATCTGGCTGACCATGC 1047
Qy 364 TCAGCATGATTGTGGGTGCCACCTGCTACGCCATGTTTCATCGGCCACGCGCACTGCCCTCA 423
Db 1048 TCAGCATGATTGTGGGTGCCACCTGCTACGCCATGTTTCATCGGCCACGCGCACTGCCCTCA 1107

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QY 424 TCCAGTCGCTGGACTCTCTCGCGCGCCAGTACACGAGAGATCAACAGAGGTGGAGCAGT 483
Db 1108 TCCAGTCGCTGGACTCTCTCGCGCGCCATATCC---AGAATACAGAGGTGGAGCAGT 1164
QY 484 ACATGTCCTTCCAAAGAGTCCAGCTGACTTCGCGCAGAGATCCAGCTACTATGAGC 543
Db 1165 ACATGTCCTTCCAAAGTCCGCGCGCAGCTTCGCGCAGAGATCCAGCTACTATGAGC 1224
QY 544 ACCGTTACAGGCGAGAGTGTTCAGAGAGACAGCATCTCGCGGAGCTCAACGGGCCCC 603
Db 1225 ACCGTTACAGGCGAGAGTGTTCAGAGAGACAGCATCTCGCGGAGCTCAACGGGCCCC 1284
QY 604 TCGGAGAGAGATCGTCAACTTCACTGCGGAGAGTGGTGGCTCCATGCCCTGTTCG 663
Db 1285 TCGGAGAGAGATGTCACTTCACTGCGGAGAGTGGTGGCTCCATGCCCTGTTCG 1344
QY 664 CCAACGCGGACCCCACTTCGTCAACGCGCATGCTGACCAAGCTCAAGTTGAGGTTCTTC 723
Db 1345 CCAATGCTGACCCCACTTCGTCAACGCGCATGCTGACCAAGCTCAAGTTGAGGTTCTTC 1404
QY 724 AGCGGGTGTACTATCATCATCGGAGAGGACCATCGGAGAGAGATGACTTCCATCCAGC 783
Db 1405 AGCGGGTGTACTTACTCATCGGAGAGGACCATCGGAGAGATGACTTCCATCCAGC 1461
QY 784 ACAGCGTGTGTCAGGCTCTCACTAAGGGCAACAGAGAGATGAAGCTGTCCGATGGCTCT 843
Db 1462 ACAGCGTGTGTCAGGCTCTCACTAAGGGCAACAGAGAGATGAAGCTGTTCGATGGCTCT 1521
QY 844 ACTTCGGGGAGATGCTGCTCTCAACCGGGCGCGCACGCGAGCGTTCGGGCTGACA 903
Db 1522 ACTTCGGAGAGATGCTGCTCTCAACCGGGCGCGCACGCGATGGCGGCGCAACA 1581
QY 904 CTTACTCGCGCTCTATTTCGTGAGCTGAGACAACTTCAACGAGAGTGTGGAGAGTACC 963
Db 1582 CTTATTCCGCGCTCTTTTCGTGAGCTGAGCTGGACAACTTCAACGAGAGTGTGGAGAGTACC 1641
QY 964 CCATGATGCGCGCGCTTCGAGACGCTGGCCATCGACCGCTGGACCGCATCGGCAAGA 1023
Db 1642 CCATGATGCGCGCGCTTCGAGACGCTGGCCATCGACCGCTGGACCGCATCGGCAAGA 1701
QY 1024 AGAATTCATCTCTCTGACAAAGTGCAGCATGACCTCAACTCGCGGCGTATTCAACAACC 1083
Db 1702 AGAATTCATCTCTCTGACAAAGTGCAGCATGACCTTAACTCGGCGGTATTCAACAACC 1761
QY 1084 AGGAGAACGCGCATCATCAGAGATCGTCAAGTACGACCGCGAGATGCTGCAGAGCCG 1143
Db 1762 AGTAAACGCGCATCATCAGAGATCGTCAAGTACGACCGCGAGATGCTGCAGAGCCG 1821
QY 1144 AGCTGGGCTCAGCGGTGGGCTCTTCCGCGCGCGCGCGCGCGCGCGCGAGTCACTTCGG 1203
Db 1822 AGCTGGG-TCAGCGCTCTGGGCTCTTCCGCGCGCGCGCGCGCGCGCGAG--GTCACTTCGG 1878
QY 1204 CCATCGGCACGCTCAGCAGCGCGCGCGCATGAGCTTCTGCGCGCA-GTGGCGCGCGCG 1262
Db 1879 CCATCGGCACGCTCAGCAGCGCGCGCGCATGAGCTTCTGCGCGCATGAGCTTCTGCGCGCGCGCGCG 1938
QY 1263 TCGTGGGCGCGCTCGGCTCGGCTCGCGCGCGCTCGTGGCGGCGGCGGCGGCGGCGG 1322
Db 1939 TCGTGGGCGCGCTCGGCTCGGCTCGGCGCGCTCGTGGCGGCGGCGGCGGCGGCGGCGG 1998
QY 1323 CACCTGCGGCGGCTCAACC 1342
Db 1999 CACCTGCGGCGGCTCAACC 2018
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RESULT 8

US-10-017-161-2369
; Sequence 2369, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA

```
; APPLICANT: ABURATANI, HIROYUKI  
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 084335/0152  
; CURRENT APPLICATION NUMBER: US/10/017,161  
; CURRENT FILING DATE: 2002-12-18  
; PRIOR APPLICATION NUMBER: JP 2001/246789  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 2430  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2369  
; LENGTH: 1966  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: source  
; LOCATION: (1)..(1966)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (201)..(1766)  
; FEATURE:  
; NAME/KEY: modified_base  
; LOCATION: (7)..(106)  
; OTHER INFORMATION: a, t, c, g, unknown or other  
; FEATURE:  
; NAME/KEY: modified_base  
; LOCATION: (139)  
; OTHER INFORMATION: a, t, c, g, unknown or other  
; FEATURE:  
; NAME/KEY: modified_base  
; LOCATION: (1915)..(1966)  
; OTHER INFORMATION: a, t, c, g, unknown or other  
; US-10-017-161-2369
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Query Match 82.7%; Score 1109.2; DB 15; Length 1966;

Best Local Similarity 95.8%; Pred. No. 9,6e-285; Mismatches 43; Indels 9; Gaps 4;
Matches 1184; Conservative 0;

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QY 4 TCGCGCTTCAACAGATCCCTCGCGGTGCTGCGCTCTCACGCTGATCCGCT 63
Db 688 TCGCGCTTCAACAGATCCCTCGCGGTGCTGCGCTCTCACGCTGATCCGCT 747
QY 64 ACATCCATCAGTGGGAGAGATCTTCCATGACCTATGACCTGGCGAGCGGCGGTATGA 123
Db 748 ACATCCACAGTGGGAGAGATCTTCCATGACCTATGACCTGGCGAGCGGCGGTATGC 807
QY 124 GATCTGCAATCTCATCAGCATGATGCTGCTCTGCGCACTGGGAGCGCTGCTGCAGT 183
Db 808 GGTTCGCAACCTCATCAGTATGATGCTGCTCTGCGCACTGGGATGGCTGCTGCAGT 867
QY 184 TCTGTGTGCCATGCTGCGAGGACTTCCCGCAACTGCTGGGTGTCCATCAATGGCATGG 243
Db 868 TCTGTGTGCCATGCTGCGAGGACTTCCCGTGCNACTGCTGGGTGTCCATCAATGGCATGG 927
QY 244 TGAACCACTCGTGGAGTGAATGTACTCTTCGCACTCTTCAAGGCGCATGAGCCATGC 303
Db 928 TGAACCACTGGTGGAGCGAACTGTATTCCTTCGCACTCTTCAAGGCGCATGAGCCATGC 987
QY 304 TGTGATCGGATACGCGCGGCGAGGATGACGAGCATGCGGACATCTGCTGACCATGC 363
Db 988 TGTGCAATGGGTATGCGCGCGGCGAGGATGACGAGCATGCGGACATCTGCTGACCATGC 1047
QY 364 TCAGCATGATTGTGGGTGCCACCTGCTAGCCATGTTTCATCGGCGCACCGCACTGCCCTCA 423
Db 1048 TCAGCATGATTGTGAGTGCCACCTGTATCGCCATGTTTCATCGGCGCACCGCACTGCCCTCA 1107
QY 424 TCCAGTTCGCTGGACTCTTCGCGCGCGCAGTACAGGAGAGATCAAGAGAGTGGAGAGT 483
Db 1108 TCCAGTTCGCTGGACTCTTCGCGCGCGCAGTACC---AGAAGTACAAAGCAGTGGAGCAGT 1164
QY 484 ACATGTCCTTCCAAAGTTCGCGCGCAGCTGACTTCGCGCAGAGATCCAGCTACTATGAGC 543
Db 1165 ACATGTCCTTCCAAAGTTCGCGCGCGCAGCTTCGCGCAGAGATCCAGCTACTATGAGC 1224
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QY 544 ACCGTTACAGGCAAGATGTTTACAGAGCAGCATCTGCGGAGCTCAACGGGCCCC 603
DB 1225 ACCGTTACAGGCAAGATGTTTACAGAGCAGCATCTGCGGAGCTCAACGGGCCCC 1284
QY 604 TCGGGAGGAGATCGTCAACTTCAACTGCGGAAGCTGGTGGCTCCATGCGCGTGTTCG 663
DB 1285 TCGGGAGGAGATGTTCAACTTCAACTGCGGAAGCTGGTGGCTCCATGCGCGTGTTCG 1344
QY 664 CCAACGCGACCCCAACTTTCGTCACGGCCATGCTGACCAAGCTCAAGTTGAGAGTCTTCC 723
DB 1345 CCAAGTCTGACCCCAACTTTCGTCACGGCCATGCTGACCAAGCTCAAGTTGAGAGTCTTCC 1404
QY 724 AGCGGGTGACTACATCATCCGGAAGCAGCATCGGGAAGATGATGTTCAATCCAGC 783
DB 1405 AGCGGGTGACTACATCATCCGGAAGCAGCATCGGGAAGATGATGTTCAATCCAGC 1461
QY 784 AGCGGGTGCTCAGCGTGCTCACTAAGGGCAACAAGGAGATGAAGCTGTCGATGGCTCCT 843
DB 1462 AGCGGGTGCTCAGCGTGCTCGCTAAGGGCAACAAGGAGATGAAGCTGTTGATGGCTCCT 1521
QY 844 ACTTCGGGAGATCTGCTGCTCAACCCGGGGCGCGCAGCGAGCTGCGGGCTGACA 903
DB 1522 ACTTCGGGAGATCTGCTGCTCAACCCGGGGCGCGCAGCGAGCTGCGGGCTGACA 1581
QY 904 CTTACTGCGCGCTCTATTTCGCTGAGGTGAGCAACTTCAACGAGTGTGGAGGAGTACC 963
DB 1582 CTTATTGCGCGCTCTTTCGCTGAGCGTGGCAACTTCAACGAGTGTGGAGGAGTACC 1641
QY 964 CATGATGCGGGCGCGCTTCGAGACGGTGGCCATCGACCGCTGGACCGCATCGGCAAGA 1023
DB 1642 CATGATGCGGGCGCGCTTCGAGACGGTGGCCATCGACCGCTGGACCGCATCGGCAAGA 1701
QY 1024 AGAATTCATCTCTCTGCAACAAGGTGACGATGACTCAACTCGGGCGTATTCAACAACC 1083
DB 1702 AGAATTCATCTCTCTGCAACAAGGTGACGATGACTCAACTCGGGCGTATTCAACAACC 1761
QY 1084 AGGAGAACCCATCATCCAGGAGATCGTCAAGTACGACCGCGAGATGTGCGAGGCGG 1143
DB 1762 AGTAGAACCCATCATCCAGGAGATCGTCAAGTACGACCGCGAGATGTGCGAGGCGG 1821
QY 1144 AGCTGGGCTCAGCGGTGGGCTCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1203
DB 1822 AGCTGGG-TCGGGCTGGGCTCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1878
QY 1204 CCATGCCACGCTGACGAGCGGGCGGCGCATGAGCT 1239
DB 1879 CCATGCCACGCTGACGAGCGGCGGTGTCATGAGCT 1914

RESULT 9
US-10-067-457-6
; Sequence 6, Application US/10067457
; Publication No. US20030082513A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharma Deutschland GmbH
; TITLE OF INVENTION: Process for identifying substances which modulate the
; FILE OF INVENTION: activity of hyperpolarization-activated cation channels
; FILE REFERENCE: AVE D-2000/A006
; CURRENT APPLICATION NUMBER: US/10/067,457
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US/09/779,587
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 3102
; TYPE: DNA
; ORGANISM: Murinae gen. sp.

Query Match 78.1%; Score 1048.6; DB 14; Length 3102;
Best Local Similarity 87.6%; Pred. No. 1.4e-268;
Matches 1173; Conservative 6; Mismatches 156; Indels 4; Gaps 3;

QY 4 TGGCGTTACCAAGATCTCTCAGCCCTCTGCGGCTGCTGCGCTCTCTCAGCGCTGATCCGCT 63
DB 931 TGGCGTTACCAAGATCTCTCAGCTCTGCTGCGGCTGCTGCGGCTATCAGCGCTCATCCGAT 990
QY 64 ACATCCATCAGTGGGAGGAGATCTTCCACATGACCTATGACCTGGCCAGCGGCTGATGA 123
DB 991 ATATCCACCACTGGGAAGAGATTTTCCACATGACCTACGACCTGGCAAGTCAAGTATGC 1050
QY 124 GGATCTGCAATCTCATCAGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 183
DB 1051 GCATCTGTAACTCTCATCAGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1110
QY 184 TCCTGGTGGCCATCTGCGAGGATCTTCCGCGCAACTGCTGGGTGCTTCCATCAATGGCATGG 243
DB 1111 TCCTGGTGGCCATCTGCAAGCTTCCCGAGCTGCTGGGTGCTTCCATCAACATGG 1170
QY 244 TGAACCACTCTGAGGATGAACTGTACTCTTTCGCACTCTTCAAGGCCATGAGCCATGTC 303
DB 1171 TGAACCACTCTGAGGAGGCTCTACTCTGTTGCGGCTCTTCAAGGCCATGAGCCATGTC 1230
QY 304 TGTGATCGGCTACGCGCGGAGCGGCGCGGAGAGCATGACGAGCATCTGGGCTGACCATGC 363
DB 1231 TGTGATCGGCTACGCGCGGAGCGGCGCGGAGAGCATGACGAGCATCTGGGCTGACCATGC 1290
QY 364 TCAGCATGATGTTGGGTGCGCACTGCTACGCCATGTTTCATCGGCGACGCCACTGCGCTCA 423
DB 1291 TCAGCATGATGTTGGGTGCGCACTGCTATGCCATGTTTCATTTGGGCGACGCCACTGCGCTCA 1350
QY 424 TCCAGTCTGCTGGAATCTCTCGCGGCGCGCACTACAGGAGAGTACAAAGCAGGTGGAGCAT 483
DB 1351 TCCAGTCTGCTGGAATCTGTCACGCGGCCATACAGGAGAGTACAAAGCAGGTGGAGCAT 1410
QY 484 ACATGCTCTTCCAAAGCTGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 543
DB 1411 ACATGCTCTTCCAAAGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1470
QY 544 ACCGTTACCAAGGCAAGATGTTTACAGGAGAGCATCTCTGCGGAGCTCAACGGGCCCC 603
DB 1471 ACCGTTACCAAGGCAAGATGTTTATGAGGAGAGATCTCTTGGGGAAGTCAACGGGCCCC 1530
QY 604 TCGGGAGGAGATCGTCAACTTCAACTGCGCGGAAGCTGGTGGCTTCCATGCGCGTGTTCG 663
DB 1531 TCGGTGAGGAGATGTTGTAACCTTCAACTGCGCGGAAGCTGGTGGCTTCCATGCGCGTGTTCG 1590
QY 664 CCAACGCGACCCCAACTTTCGTCAGGCGCATGCTGACCAAGCTCAAGTTCGAGGCTCTTCC 723
DB 1591 CCAATGACAGCCCAACTTTCGTCAGGCGCATGCTGACCAAGCTCAAAATTTGAGGCTCTTCC 1650
QY 724 AGCGGGTGACTACATCATCCGGAAGCAGCATCGGGAAGATGATGTTCTCATCCAGC 783
DB 1651 AGCGGGTGAGATTTACATCATCCGAGAGGGGAGCCATCGGGAAGAGATGATGTTCTATCCAGC 1710
QY 784 ACGGCTGCTCAGCGTGTCTCACTAAGGCAACAAGGAGATGAAGCTGCTCCGATGGCTCCT 843
DB 1711 ATGGGTGCTGAGCGTGTCTCAACAGGCAACAAGGAGATGAGCTGTCGATGCTCCT 1770
QY 844 ACTTCGGGAGATCTGCTGCTCAACCCGGGGCGCGCGCAGCGGAGCGGTGCGGCTGACA 903
DB 1771 ATTTGGGGAGATCTGCTTGTCTCAGAGGGGCGCGCGGTACGCGCCAGCGTGGAGCTGACA 1830
QY 904 CCTACTGCGGCTCTATTTCGCTGAGCGGTGAGCAACTTCAACGAGTGTCTGGAGGAGTACC 963
DB 1831 CCTACTGCGGCTCTTACTCACTGAGTGTGGACAATTTCAACGAGTGTCTGGAGGATACC 1890
QY 964 CCATGATCGCGCGGCTTTCGAGACGGTGGCCATCGACCGCTGCGACCGCATCGGCAAGA 1023
DB 1891 CCATGATCGCGGCTGCTTTGAGACTGTGGCTATTGACCGGCTAGATGCTGATAGGCAAGA 1950
QY 1024 AGAATTCATCTCTCTGCAACAAGGTGACGATGACTCAACTCGGGCGGTATTCAACAACC 1083
DB 1951 AGAATTCATCTCTCTGCAACAAGGTGACGATGACTCAAGTTCAGGCTGAGTGTGTTCAACAACC 2010

1084 AGGAGAACCCATCATCCAGGAGATCTCAAGTACGACCGCGAGATGTGACGAGCGG 1143
1085 |||||
2011 AGGAGAAATCCATCATCCAGGAGATGTCAAAATATACCGTGGATGTGACGAGCGAG 2070
2012 |||||
1144 AGCTGGGCTCAGCGGCTGGGCTCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1203
1204 |||||
2071 AGCTTGGC-CAGCGTGTGGGCTCTTCCACACCGCGCGCGCGCGCGCGCGCGCG 2127
2072 |||||
1204 CCATGCCACCGTGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1262
1205 |||||
2128 CCATTGCCACCGTGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2187
2129 |||||
1263 TCGTGGGCGCGTGGGCGCTGGGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1322
1264 |||||
2188 TCGTGGGCGCGTGGGCGCTGGGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2247
2189 |||||
1323 CACCTGCHGCGCGCTCACCC 1341
2248 TGGCTCTCGAGCGCTCGCC 2266

RESULT 10
US-10-311-795-5
; Sequence 5, Application US/10311795
; Publication No. US20040033943A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham plc
; TITLE OF INVENTION: New Use
; FILE REFERENCE: P32614
; CURRENT APPLICATION NUMBER: US/10/311,795
; PRIORITY FILING DATE: 2002-12-19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 4751
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-311-795-5

Query Match 69.1%; Score 927.2; DB 18; Length 4751;
Best Local Similarity 84.7%; Pred. No. 2.9e-236;
Matches 1040; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

4 TGGCTTACCAAGATCCTGAGCTCTGAGCTCTTACGCTCTTACGCTCTTCCGCTCATTCGAT 2185
2126 TCGCTTACCAAGATCCTGAGCTCTTACGCTCTTACGCTCTTACGCTCTTCCGCTCATTCGAT 2185

64 ACATCCATCAGTGGGAGAGATCTTCCACATGACCTATGACCTGGCGCGCGCGCTGATGA 123
2186 ATATTCCACCATGGGAGAGATCTTCCACATGACCTATGACCTGGCGCGCGCGCTGATGA 2245

124 GGATCTGCAATCTCATCAGCATGATGCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG 183
2246 GCATCTGCAATCTCATCAGCATGATGCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG 2305

184 TCCTGGTCCCATGCTGAGAGATCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 243
2306 TCCTGGTCCCATGCTGAGAGATCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2365

244 TGAACCACTCTGGGAGTGAAGTCTTCTGCGACCTTCTCAAGGCGCATGAGCCACATGC 303
2366 TGAACCACTCTGGGAGTGAAGTCTTCTGCGACCTTCTCAAGGCGCATGAGCCACATGC 2425

304 TGTGATCGGCTAGCG 363
2426 TGTGATCGGCTAGCG 2485

364 TCAGCATGATGTGGGTGCCACCTGTCTAGCGCATGTTTCATCGCGCGCGCGCGCGCGCG 423
2486 TCAGCATGATGTGGGTGCCACCTGTCTAGCGCATGTTTCATCGCGCGCGCGCGCGCGCG 2545

424 TCCAGTCCGTGAGTCTCTCG 483

2546 TCCAGTCCGTGAGTCTCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2605
484 ACATGTCTCTCCACAAAGTGCAGCTGACTTCCCGCGCGCGCGCGCGCGCGCGCGCGCG 543
2606 ACATGTCTCTCCACAAAGTGCAGCTGACTTCCCGCGCGCGCGCGCGCGCGCGCGCGCG 2665
544 ACCGTTCACAGGCGCAAGATGTTTACGAGGAGCAGCATCTCTGGCGCGCGCGCGCGCG 603
2666 ACCGTTCACAGGCGCAAGATGTTTACGAGGAGCAGCATCTCTGGCGCGCGCGCGCGCG 2725
604 TCGCGGAGGAGATCTGCTCAACTTCAACTCGCGGAGCTGTGTGCTCTCCATGCGCGCTT 663
2726 TCGCGGAGGAGATCTGCTCAACTTCAACTCGCGGAGCTGTGTGCTCTCCATGCGCGCT 2785
664 CCAACCG 723
2786 CCAATGCG 2845
724 AGCCGGGTGATCATCATCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 783
2846 AGCCTGGGCG 2905
784 AGCGGTGCTGAGCGCTGCTCACTAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 843
2906 ATGGGTGCTGAGCGCTGCTCACTAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2965
844 ACTTCGGGAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 903
2966 ACTTCGGGAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3025
904 CCTACTGCGCGCTCTATTCGCTGAGCGTGGAACAATTCAACGAGGTGCTGGAGGATACC 963
3026 CCTACTGCGCGCTCTATTCGCTGAGCGTGGAACAATTCAACGAGGTGCTGGAGGATACC 3085
964 CCATGATGCGCGCGCGCTTCCGAGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1023
3086 CCATGATGCGCGCGCGCTTCCGAGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3145
1024 AGAATTCATCTCTCTGCAAGGTCGACGATGACCTCAACTCGCGCGGTATTCACAAACC 1083
3146 AGAATTCATCTCTCTGCAAGGTCGACGATGACCTCAACTCGCGCGGTATTCACAAACC 3205
1084 AGGAGAACCCATCATCCAGGAGATCTCAAGTACGACCGCGCGAGATGTGTCAGCAGCGG 1143
3206 AGGAGAACCCATCATCCAGGAGATCTCAAGTACGACCGCGCGAGATGTGTCAGCAGCGG 3265
1144 AGCTGGGCTCAGCGCGTGGGCTCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1203
3266 ACCGCTCCAGGCTGCTGCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3325
1204 CCATGCCACCGCTGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1231
3326 TGATCAGGCG 3353

RESULT 11
US-10-067-457-4
; Sequence 4, Application US/10067457
; Publication No. US20030082513A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharma Deutschland GmbH
; TITLE OF INVENTION: Process for identifying substances which modulate the
; TITLE OF INVENTION: activity of hyperpolarization-activated cation channels
; FILE REFERENCE: AVE D-2000/A006
; CURRENT APPLICATION NUMBER: US/10/067,457
; PRIORITY FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US/09/779,587
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 5065
; TYPE: DNA

; ORGANISM: Homo sapiens		69.1%; Score 927.2; DB 14; Length 5065;	
US-10-067-457-4		Best Local Similarity 84.7%; Pred. No. 2.9e-236;	
		Matches 1040; Conservative 0; Mismatches 188; Indels 0; Gaps 0;	
QY	4	TGGCTTACCAAGATCTCAGCCTCTCGGCTCTCGGCTCTCAGCCTGATCCGCT	63
Db	1696	TCCGCTTCAGAAATCTCAGCCTCTTACGCTCTTACGCTCTTCCGCTCTCCGCTCATTCGAT	1755
QY	64	ACATCCATCAGTGGGAGGAGATCTTCCACATGACCTATGACCTGGCGACGCGGTGATGA	123
Db	1756	ATATTACCAAGTGGGAGGAGATCTTCCACATGACCTTACGCTTGGCAGCGCGGTGGTGC	1815
QY	124	GGATCTGCAATCTCATCAGATGATGCTGCTCTTGCACATGGGACGGCTGCCGTGCACT	183
Db	1816	GCATCGTGAACCTCATCGGCATGATGCTCTGCTCTGCCACTGGGAGCGCTGCCGTGCACT	1875
QY	184	TCTGTGTGCCATGCTGCGAGGACTTCCCGGCAACTGCTGGGTGTCCATCAATGGCATGG	243
Db	1876	TCTGTGTGCCATGCTGCGAGGACTTCCCGGCAACTGCTGGGTGTCCATCAATCAACATGG	1935
QY	244	TGAACCACTCGTGGAGTGAATGCTACTCTTCTTGGCACTTCTCAAGGCAATGAGCCATGC	303
Db	1936	TGNACAACTCTGGGGAAGCAGTACTCTTACGCGCTCTTCAAGGCCATGAGCCATGC	1995
QY	304	TGTGCATCGGTTACGCCCGCAGGCGCCGAGAGCATGACGACATCTGGCTGACCATGC	363
Db	1996	TGTGCATCGGTTACGCCCGCAGGCGCCGTTGGCATGTCCGAGCTTGGCTCACCATGC	2055
QY	364	TCAGCATGATTTGGGTGCCACCTGCTAGCCCATGTTTCATCGGCCACGCCACTGCCCTCA	423
Db	2056	TCAGCATGATTCGTTGGGTGCCACCTGCTAGCCCATGTTTCATCGGCCACGCCACTGCCCTCA	2115
QY	424	TCAGTTCGCTGACTCTCTCGCGCGCAGTACAGGAGAAAGTACAGAGGTGGAGCAGT	483
Db	2116	TCAGTTCGCTGACTCTCTCGCGCGCAGTACAGGAGAAAGTACAGAGGTGGAGCAGT	2175
QY	484	ACATGTCCTTCCAAAGCTGCCAGTCTGACTTCGCGCAGAAAGTCCACGACTACTATGAGC	543
Db	2176	ACATGTCCTTCCAAAGCTGCCAGTCTGACTTCGCGCAGAAAGTCCACGACTACTATGAGC	2235
QY	544	ACGTTTACAGGCAAGATGTTTGACGAGCAAGCATCTGGCGAGGCTCAACGGGCCCC	603
Db	2236	ACGCTTACAGGCAAGATGTTTGACGAGGAGCATCTCGCGAGGACTTAAAGCGAGCCCC	2295
QY	604	TGCGGAGAGATCGTCAACTTCACTTCCGGAAGCTGGTGGCTCCATGCCGCTGTTGG	663
Db	2296	TGCGGAGAGATCATCAACTTAACTTTCGGAAGCTGGTGGCTCCATGCCACTGTTTG	2355
QY	664	CCAAACCGACCCCACTTCGTACGGCCATGCTGACCAAGCTCAAGTTTCGAGGCTTCC	723
Db	2356	CCAAATCGGACCCCACTTCGTGACGTCTCATGTCGACCAAGCTGCGTTTCGAGGCTTCC	2415
QY	724	AGCGGGGTACTATCATCTCCGGAAGGCAACCATCGGGAAGAGATGTAATTCATCCAGC	783
Db	2416	AGCCTGGGACTATCATCTCCGGAAGGCAACCATTCGGAAGAGATGTAATTCATCCAGC	2475
QY	784	ACGCGGTGTTCAGCGTCTCACTTAAGGGCAACAAGGAGATGAAGCTTCCGATGGCTCT	843
Db	2476	ATGGCGGTGTTCAGCGTCTCACTTAAGGGCAACAAGGAGATGAAGCTTGGCGGAGCTCT	2535
QY	844	ACTTCGGGAGATCTGCTCTCACCCGGGGCGCGCACGGGAGCGTGGGGCTGACA	903
Db	2536	ACTTTGAGAGATCTGCTCTGACCCGGGGCGCGCACAGCCAGCGTGGGGCGGACA	2595
QY	904	CCTACTGCCGCTCTATTTCGTGAGCGTGGACAATTTCAACAGAGTGTCTGGAGAGTACC	963
Db	2596	CCTACTGCCGCTCTATTTCGTGAGCGTGGACAATTTCAATGAGTGTCTGGAGAGTACC	2655
QY	964	CCATGATGGGGCGGCTTTCGAGACGGTGGCCATCGACCGCTGGACCGCATCGGCAAGA	1023

RESULT 12

US-10-276-774-973

; Sequence 973, Application US/10276774

; Publication No. US20040053245A1

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc.

; APPLICANT: Tang, Y, Tom et al

; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides

; FILE REFERENCE: 21272-030

; CURRENT APPLICATION NUMBER: US/10/276,774

; CURRENT FILING DATE: 2002-11-18

; PRIOR APPLICATION NUMBER: 09/560,875

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: 09/496,914

; PRIOR FILING DATE: 2000-02-03

; NUMBER OF SEQ ID NOS: 2700

; SOFTWARE: Custom

; SEQ ID NO 973

; LENGTH: 5499

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-276-774-973

Query Match 69.1%; Score 927.2; DB 18; Length 5499;

Best Local Similarity 84.7%; Pred. No. 3e-236; Indels 0; Gaps 0;

Matches 1040; Conservative 0; Mismatches 188;

QY	4	TGCGCTTCCACCAAGATCTCAGCCTCTCGGCTCTCGGCTCTCAGCCTGATCCGCT	63
Db	2128	TCCGCTTCCACCAAGATCTCAGCCTCTTACGCTCTTACGCTCTTCCGCTCATTCGAT	2187
QY	64	ACATCCATCAGTGGGAGGAGATCTTCCACATGACCTATGACCTGGCGAGCGGGTATGA	123
Db	2188	ATATTACCAAGTGGGAGGAGATCTTCCACATGACCTTACGACCTGCGCGAGCGCGTGGTGC	2247
QY	124	GGATCTGCAATCTCATCAGCATGATGCTGCTCTGCGCACTTGGACCGCTGCCCTGCAGT	183
Db	2248	GCATCGTGAACCTCATCGGCATGATGCTCTGCTCTGCGCACTTGGACCGCTGCCCTGCAGT	2307
QY	184	TCCTGGTGGCCATGCTGCGAGGACTTCCCGCGCAACTGCTGGGTGTCCATCAATGGCATGG	243
Db	2308	TCCTGGTGGCCATGCTGCGAGGACTTCCCTGAGCAGTCTGCTGGGTGTCCATCAACACATGG	2367
QY	244	TGAACCACTCGTGGAGTGAATGTAATCTCTTTCGCACTTTCAAGGCCATGAGCCCATGC	303
Db	2368	TGAACCACTCTGGGGGAAGCAGTACTCTTACGCGCTCTTCAAGGCCATGAGCCCATGC	2427
QY	304	TGTGATCGGTTACGCCCGGCGGAGAGCATGACGACATCTGGCTGACCATGC	363
Db	2428	TGTGATCGGTTACGCCCGGCGGAGGCGCGGTGGGATGTCGAGCATGCTGGCTTCAACATGC	2487
QY	364	TCAGCATGATTTGGGTGCCACCTCTACTAGCGCATGTTTCATCGGCCACGCCACTGCCCTCA	423
Db	2488	TCAGCATGATTTGGGTGCCACCTCTACTAGCGCATGTTTCATTTGGCCACGCCACTGCCCTCA	2547

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